

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 54.5455 Seconds
(without alignments)
125.735 Million cell updates/sec

Title: US-10-758-165a-1
Perfect score: 81
Sequence: 1 RNDSP1QTDQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	81	100.0	15	ADR10601	Adr10601 Dog Ige e
2	81	100.0	312	AAV79995	Aav79995 Dog immun
3	81	100.0	417	AAW23067	Aaw23067 Canine Ig
4	81	100.0	426	AAW97753	Aaw97753 Canine Ig
5	81	100.0	426	ABP96583	Abp96583 Dog Ige h
6	53	65.4	15	ADR10607	Adr10607 Pig Ige e
7	53	65.4	567	ABP96588	Abp96588 Pig Ige h
8	48	59.3	15	ADR10602	Adr10602 Cat Ige e
9	48	59.3	431	ADG73237	Adg73237 Cat immun
10	48	59.3	496	ABP96580	Abp96580 Cat Ige h
11	48	59.3	496	ABU09338	Abu09338 Feline Ig
12	48	59.3	496	ABU09336	Abu09336 Feline Ig
13	48	59.3	496	ADG73251	Adg73251 Cat parti
14	48	59.3	496	ADG73225	Adg73225 Cat parti
15	43	53.1	1633	ABU42513	Abu42513 Proteine
16	42	51.9	1067	ABB91309	Abb91309 Herbicida
17	41	50.6	15	ADR10603	Adr10603 Horse Ige
18	41	50.6	151	AAU57418	Aau57418 Propionib
19	41	50.6	151	ABM53937	Abm53937 Propionib
20	41	50.6	424	AAW50103	Aaw50103 Equine Ig
21	41	50.6	424	AAW50104	Aaw50104 Equine Ig
22	41	50.6	533	ABP39208	Abp39208 Staphyloc
23	41	50.6	533	ADS05754	Ads05754 Staphyloc

24	41	50.6	566	9	AED15438	Aed15438 Equine Pr
25	41	50.6	566	10	AEE88000	Aee88000 Human pro
26	41	50.6	569	6	ABP96585	Abp96585 Horse Ige
27	40	49.4	356	4	ABB64299	Abb64299 Drosophil
28	40	49.4	358	8	ADY09532	Ady09532 Plant ful
29	40	49.4	555	6	ADA24243	Ada24243 Pseudomon
30	40	49.4	632	7	ABM90457	Abm90457 Rice abio
31	40	49.4	632	7	ABM85909	Abm85909 Rice abio
32	40	49.4	659	10	AEF24334	Aef24334 Esterase
33	40	49.4	667	6	ADA33007	Ada33007 Acinetoba
34	40	49.4	1180	3	AAB01845	Aab01845 Haemophil
35	40	49.4	1188	3	AAB01844	Aab01844 Haemophil
36	40	49.4	2349	6	AAO16359	Aao16359 Human tra
37	40	49.4	2400	4	ABG20278	Abg20278 Novel hum
38	40	49.4	2415	4	ABG20279	Abg20279 Novel hum
39	39	48.1	226	8	ADRA4996	Adra4996 SnsAG3 an
40	39	48.1	276	3	AAG08697	Aag08697 Arabidops
41	39	48.1	276	3	AAG42639	Aag42639 Arabidops
42	39	48.1	281	8	ADI28921	Adi28921 Sarcocyst
43	39	48.1	281	8	ADR44989	Adr44989 Sarcocyst
44	39	48.1	294	3	AAG08696	Aag08696 Arabidops
45	39	48.1	294	3	AAG42638	Aag42638 Arabidops

ALIGNMENTS

RESULT 1	ADRI0601	ADRI0601 standard; peptide; 15 AA.
XX	AC	ADRI0601;
XX	XX	21-OCT-2004 (first entry)
XX	XX	Dog Ige epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
XX	XX	Antiaethmatic; Antiallergic; Immunosuppressive; Ige; dog; asthma;
XX	XX	anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX	OS	Canis familiaris.
XX	XX	W02004065936-A2.
XX	XX	05-AUG-2004.
XX	XX	15-JAN-2004; 2004WO-US003566.
XX	XX	16-JAN-2003; 2003US-0440472P.
XX	XX	(UYNC-) UNIV NORTH CAROLINA STATE.
XX	XX	Hammerberg B;
XX	XX	WPI; 2004-593545/57.
XX	XX	Novel antibody that specifically binds to mammalian Ige epitope, useful
XX	XX	for testing an allergen reactivity of Ige sample, detecting mammalian Ige
XX	XX	or treating asthma or anaphylactic shock.
XX	XX	Example 6; Page 9; 14pp; English.
XX	XX	The present invention relates to a novel monoclonal antibody (I) that
XX	XX	specifically binds to a mammalian Ige epitope, where the epitope is
XX	XX	between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige.
XX	XX	(I) is useful for testing an allergen reactivity of an Ige sample. The
XX	XX	allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX	XX	and corn allergens. The sample is a biological sample collected from a
XX	XX	dog, cat or horse. (I) is also useful for detecting mammalian Ige and for
XX	XX	treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX	XX	antibodies recognise epitopes on canine Ige corresponding to amino acid
XX	XX	residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX	XX	canine Ige epsilon-chain. Recognition of epsilon-chains from Ige from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
 |||||
 Db 1 RNDSPQTQDQYTTTG 15

RESULT 2

AAV79995 ID AAV79995 standard; protein; 312 AA.

XX AC AAV79995;

XX 15-MAY-2000 (first entry)

XX DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX OS Canis sp.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy.

XX Example 1; Page 66-68; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IgE, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AAV79994 to AA780084 represent amino acid
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 312 AA;

Query Match 100.0%; Score 81; DB 3; Length 312;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
 |||||
 Db 255 RNDSPQTQDQYTTTG 269

RESULT 3

AAW23067 ID AAW23067 standard; protein; 417 AA.

XX AC AAW23067;

XX 30-JUN-2005 (revised)

DT 16-JUN-2005 (revised)

DT 19-FEB-1998 (first entry)

XX Canine IgE heavy chain constant region (exon 1-4 product).

XX IgE; immunoglobulin; antibody; heavy chain constant region; allergy;
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

XX OS Canis familiaris.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX WO9730156-A2.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US002322.

XX 14-FEB-1996; 96US-00601197.

XX (IDEX-) IDEXX LAB INC.

XX Mermer B, Harris RA, Siefring AE;

XX WPI; 1997-425031/39.

XX N-PSDB; AAT79278.

XX Isolated canine IgE heavy chain constant region DNA - useful to develop
 PT products for treatment of canine allergies and for immunomodulation in
 PT dogs.

XX Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to
 CC treat Type I immediate hypersensitivity, and for immunomodulation

CC Revised record issued on 30-JUN-2005 : Typo in comments
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 81; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
 |||||
 Db 352 RNDSPQTQDQYTTTG 366

RESULT 4
 AAR97753
 ID AAR97753 standard; protein; 426 AA.

AC AAR97753;
 XX
 DT 28-AUG-1996 (first entry)
 DE Canine IgE.

XX IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
 XX
 OS Canis familiaris.

XX WO9614867-A1.

XX
 XX 23-MAY-1996.

XX 03-NOV-1995; 95WO-US013795.
 XX
 PR 09-NOV-1994; 94US-00336583.
 PR 09-NOV-1994; 94US-00336891.

XX (MERI) MERCK & CO INC.
 XX
 XX Hollis GF, Patel MD;
 XX WPI; 1996-277321/28.
 DR N-PSDB; AAT29824.

XX New DNA encoding canine IgE and IgA - useful in vaccines, anti-sense
 PT therapy, assays, drug screening, etc.
 XX Claim 11; Page 29-30; 49pp; English.

XX The canine IgE amino acid sequence (AAR97753) was deduced from an
 CC isolated gene (AAT29824) obt'd. from a canine liver DNA library. The
 CC cloning of the IgE gene allows prodn. of large quantities of recombinant
 CC IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE
 CC can be used in drug development (e.g. small molecule screening, assay
 CC development and anti-IgE antibody generation). Fragments of IgE can be
 CC used in vaccines or to prevent IgE-mediated hypersensitivity. The new
 CC sequence information permits targeted modulation of IgE-mediated immune
 CC responses

XX Sequence 426 AA;

Query Match 100.0%; Score 81; DB 2; Length 426;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
 |||||
 Db 357 RNDSPQTQDQYTTTG 371

RESULT 5
 ABP96583
 ID ABP96583 standard; protein; 426 AA.

XX
 AC
 XX

ABP96583;

28-MAY-2003 (first entry)

Dog IgE heavy chain amino acid sequence SEQ ID NO:28.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KW urticaria hives.

XX Canis familiaris.

OS WO2003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
 XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IgE, by identifying peptide eliciting CTL response to IgE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.

XX Example 7; Page 152-154; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IgE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IgE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions;
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IgE, and in
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IgE heavy chain amino acid
 CC sequence, which is given in an example from the present invention

XX Sequence 426 AA;

Query Match 100.0%; Score 81; DB 6; Length 426;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
 |||||
 Db 357 RNDSPQTQDQYTTTG 371

```

RESULT 6
ID ADR10607 standard; peptide; 15 AA.
AC ADR10607;
XX
XX 21-OCT-2004 (first entry)
DT
XX
DE DE Pig IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.
XX
XX Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW pig.
XX
XX Sus scrofa.
OS
XX WO2004065936-A2.
PN
XX 05-AUG-2004.
PD
XX 15-JAN-2004; 2004WO-US003566.
XX
XX 16-JAN-2003; 2003US-0440472P.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IgE epitope, useful
PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IgE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
CC (I) is useful for testing an allergen reactivity of an IgE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IgE corresponding to amino acid
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE. The present sequence is the
CC pig IgE 5.91 recognition site.
XX
XX Sequence 15 AA;
SQ
Query Match 65.4%; Score 53; DB 8; Length 15;
Best Local Similarity 57.1%; Pred. No. 0.044;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTT 14
|||:|:|:|:|
Db 1 RNDAPVQADRHSST 14

RESULT 7
ABP96588
ID ABP96588 standard; protein; 567 AA.
XX
XX ABP96588;
AC
XX
XX 28-MAY-2003 (first entry)
DT
XX
DE DE Pig IgE heavy chain amino acid sequence SEQ ID NO:33.
XX
XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
KW immune response; major histocompatibility complex; MHC; immunogenic;
KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KW urticaria hives.
XX
XX Sus scrofa.
OS
XX WO2003015716-A2.
PN
XX 27-FEB-2003.
PD
XX 08-AUG-2002; 2002WO-US026986.
XX
XX 13-AUG-2001; 2001US-0312120P.
XX
XX (IGET-) IGE THERAPEUTICS INC.
PA
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX WPI; 2003-268242/26.
XX
XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IgE, by identifying peptide eliciting CTL response to IgE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX
XX Example 7; Page 164-167; 187pp; English.
XX
XX The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IgE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IgE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IgE, and in
CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IgE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
XX Sequence 567 AA;
SQ
Query Match 65.4%; Score 53; DB 6; Length 567;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTT 14
|||:|:|:|:|
Db 499 RNDAPVQADRHSST 512

RESULT 8
ADR10602
ID ADR10602 standard; peptide; 15 AA.
XX

```

```

AC ADR10602;
XX
DT 21-OCT-2004 (first entry)
XX
DE Cat IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.
XX
KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW cat.
XX
OS Felis catus.
XX
PN W02004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hammerberg B;
XX
DR WPI; 2004-593545/57.
XX
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IgE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
CC (I) is useful for testing an allergen reactivity of an IgE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IgE corresponding to amino acid
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE. The present sequence is the
CC cat IgE 5.91 recognition site.
XX
SQ Sequence 15 AA;
Query Match 59.3%; Score 48; DB 8; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14
|||:|:|
Db 2 NDSFVRTEQQATT 14

RESULT 9
ADG73237
ID ADG73237 standard; protein; 431 AA.
XX
AC ADG73237;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cat immunoglobulin E (IgE) constant region.
XX
KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
KW immune response; IgE-mediated response; allergy; cat; constant region.
XX

```

```

OS Felis catus.
XX
PN US2003216565-A1.
XX
PD 20-NOV-2003.
XX
PF 07-APR-2003; 2003US-00409772.
XX
PR 07-JAN-1999; 99US-0115033P.
PR 07-JAN-2000; 2000US-00479614.
XX
PA (MCCA/) MCCALL C.
PA (WEBE/) WEBER E..
XX
PI McCall C, Weber E;
XX
DR WPI; 2004-010802/01.
DR N-PSDB; ADG73236.
XX
PT New isolated nucleic acid molecule encoding a portion of a feline IgE
PT heavy chain protein, useful for treating and/or eliciting feline immune
PT responses for IgE-mediated responses, such as allergies.
XX
PS Claim 12; SEQ ID NO 14; 44pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC portion of a feline IgE heavy chain protein. The methods and compositions
CC of the present invention are useful for eliciting feline immune responses
CC for and/or treating IgE-mediated responses, such as allergies. This is
CC the amino acid sequence of a cat immunoglobulin E (IgE) constant region.
XX
SQ Sequence 431 AA;
Query Match 59.3%; Score 48; DB 8; Length 431;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14
|||:|:|
Db 363 NDSFVRTEQQATT 375

RESULT 10
ABP96580
ID ABP96580 standard; protein; 496 AA.
XX
AC ABP96580;
XX
DT 28-MAY-2003 (first entry)
XX
DE Cat IgE heavy chain amino acid sequence SEQ ID NO:25.
XX
KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
KW immune response; major histocompatibility complex; MHC; immunogenic;
KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KW urticaria hives.
XX
OS Felis catus.
XX
PN W02003015716-A2.
XX
PD 27-FEB-2003.
XX
PF 08-AUG-2002; 2002WO-US026986.
XX
PR 13-AUG-2001; 2001US-0312120P.
XX
PA (IGET-) IGE THERAPEUTICS INC.
XX
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;

```

XX WPI; 2003-268242/26.
 DR
 XX
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IgE, by identifying peptide eliciting CTL response to IgE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.
 XX
 PS Example 7; Page 145-147; 187pp; English.
 XX
 CC The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IgE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented Igs peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC Igs peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
 CC vasotropic, dermatological, anti-inflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IgE, and in
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IgE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 XX
 SQ Sequence 496 AA;
 Query Match 59.3%; Score 48; DB 6; Length 496;
 Best Local Similarity 61.5%; Pred. No. 14;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NDSPIQTDQYTTT 14
 ||||:|:|:
 Db 428 NDSFVRTEQQATT 440
 RESULT 11
 ABU09338
 ID ABU09338 standard; protein; 496 AA.
 XX
 AC ABU09338;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Feline IgE epsilon heavy chain #2.
 XX
 KW Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
 KW IgE-mediated immune response; allergy; neoplasia; vaccine technology;
 KW antibody technology; antiallergic; antiparasitic; cytostatic.
 XX
 OS Felis catus.
 XX
 FH Key Location/Qualifiers
 FT 66. .496
 FT /note= "This sequence is given as SEQ ID No:14 and is
 FT specifically claimed in Claim 12"
 FT 284. .309
 FT /note= "This sequence is given as SEQ ID No:11 and is
 FT specifically claimed in Claim 9"
 FT 288. .305
 FT /note= "This sequence is given as SEQ ID No:8 and is
 FT specifically claimed in Claim 10"
 FT 291. .302
 FT /note= "This sequence is given as SEQ ID No:5 and is
 FT specifically claimed in Claim 11"
 XX
 PN US2003013183-A1.
 XX
 PD 16-JAN-2003.
 XX
 PF 07-JAN-2000; 2000US-00479614.
 XX
 PR 07-JAN-1999; 99US-0115033P.
 XX
 XX (MCCA/) MCCAII C.
 XX (WEBE/) WEBER E.
 XX
 PI Mccall C, Weber E;

PI Mccall C, Weber E;
 XX
 DR WPI; 2003-391997/37.
 DR N-PSDB; ABX95715.
 XX
 PT New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
 PT light chain protein, useful for treating feline IgE-mediated responses
 PT e.g. allergies, parasitic infections or neoplasia.
 XX
 PS Claim 1; Page 37-39; 45pp; English.
 XX
 CC The present invention relates to the isolation of feline immunoglobulin E
 CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
 CC polynucleotide sequences encoding them. The sequences of the invention
 CC are useful for treating feline IgE-mediated immune responses (e.g.
 CC allergies, parasitic infections or neoplasia), in vaccine technology,
 CC small molecule/antibody technology, molecular biology, and various
 CC immunological techniques related to feline IgE and its functions. The
 CC present sequence represents feline IgE epsilon heavy chain #2
 XX
 SQ Sequence 496 AA;
 Query Match 59.3%; Score 48; DB 6; Length 496;
 Best Local Similarity 61.5%; Pred. No. 14;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NDSPIQTDQYTTT 14
 ||||:|:|:
 Db 428 NDSFVRTEQQATT 440
 RESULT 12
 ABU09336
 ID ABU09336 standard; protein; 496 AA.
 XX
 AC ABU09336;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Feline IgE epsilon heavy chain #1.
 XX
 KW Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
 KW IgE-mediated immune response; allergy; neoplasia; vaccine technology;
 KW antibody technology; antiallergic; antiparasitic; cytostatic.
 XX
 OS Felis catus.
 XX
 FH Key Location/Qualifiers
 FT 66. .496
 FT /note= "This sequence is given as SEQ ID No:14 and is
 FT specifically claimed in Claim 12"
 FT 284. .309
 FT /note= "This sequence is given as SEQ ID No:11 and is
 FT specifically claimed in Claim 9"
 FT 288. .305
 FT /note= "This sequence is given as SEQ ID No:8 and is
 FT specifically claimed in Claim 10"
 FT 291. .302
 FT /note= "This sequence is given as SEQ ID No:5 and is
 FT specifically claimed in Claim 11"
 XX
 PN US2003013183-A1.
 XX
 PD 16-JAN-2003.
 XX
 PF 07-JAN-2000; 2000US-00479614.
 XX
 PR 07-JAN-1999; 99US-0115033P.
 XX
 XX (MCCA/) MCCAII C.
 XX (WEBE/) WEBER E.
 XX
 PI Mccall C, Weber E;

```
XX WPI; 2003-391997/37.
DR N-PSDB; ABX95713.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
XX Claim 1; Page 24-25; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #1
XX
XX Sequence 496 AA;
SQ
Query Match 59.3%; Score 48; DB 6; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 NDSPIQTDQYTTT 14
Db 428 NDSFVRTEQQATT 440
RESULT 13
ADG73251
ID ADG73251 standard; protein; 496 AA.
AC ADG73251;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat partial immunoglobulin E (IgE) heavy chain #2.
XX
XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
XX immune response; IgE-mediated response; allergy; cat; heavy chain.
XX
XX Felis catus.
XX
XX US2003216565-A1.
XX
XX 20-NOV-2003.
XX
XX 07-APR-2003; 2003US-00409772.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX (MCCA/) MCCALL C.
XX (WEBE/) WEBER E.
XX
XX McCall C, Weber E;
XX
XX WPI; 2004-010802/01.
XX N-PSDB; ADG73250.
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IgE
XX heavy chain protein, useful for treating and/or eliciting feline immune
XX responses for IgE-mediated responses, such as allergies.
XX
XX Claim 8; SEQ ID NO 29; 44pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX portion of a feline IgE heavy chain protein. The methods and compositions
XX of the present invention are useful for eliciting feline immune responses
XX for and/or treating IgE-mediated responses, such as allergies. This is
XX the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
XX chain.
XX
XX Sequence 496 AA;
SQ
Query Match 59.3%; Score 48; DB 8; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 NDSPIQTDQYTTT 14
Db 428 NDSFVRTEQQATT 440
RESULT 15
ABU42513
ID ABU42513 standard; protein; 1633 AA.
XX
```

AC ABU42513;
XX
XX DT 19-JUN-2003 (first entry)
XX
XX DE Protein encoded by Prokaryotic essential gene #28040.
XX
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX OS Staphylococcus epidermidis.
XX
XX PN WO200277183-A2.
XX
XX PD 03-OCT-2002.
XX
XX PF 21-MAR-2002; 2002WO-US009107.
XX
XX PR 21-MAR-2001; 2001US-00815242.
XX
XX PR 06-SEP-2001; 2001US-00948993.
XX
XX PR 25-OCT-2001; 2001US-0342923P.
XX
XX PR 08-FEB-2002; 2002US-00072851.
XX
XX PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX DR WPI; 2003-029926/02.
XX
XX DR N-PSDB; ACA46383.
XX
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX
XX PT for homologous nucleic acids required for cellular proliferation to
XX
XX PT isolate candidate molecules for rational drug discovery programs.
XX
XX PS Claim 25; SEQ ID NO 70437; 1766pp; English.
XX
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX
XX CC the 6213 antisense sequences given in the specification where expression
XX
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX
XX CC polypeptide or its fragment whose expression is inhibited by the
XX
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX
XX CC proliferation or the activity of a gene in an operon required for
XX
XX CC proliferation; (7) identifying a compound that influences the activity of
XX
XX CC the gene product or that has an activity against a biological pathway
XX
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX
XX CC identifying a gene required for cellular proliferation or the biological
XX
XX CC pathway in which a proliferation-required gene or its gene product lies
XX
XX CC or a gene on which the test compound that inhibits proliferation of an
XX
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX
XX CC to which each of the strains is present in a culture or collection of
XX
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX
XX CC identifying proteins or screening for homologous nucleic acids required
XX
XX CC for cellular proliferation to isolate candidate molecules for rational
XX
XX CC drug discovery programs, or for screening homologous nucleic acids
XX
XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX
XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
XX
XX CC the target prokaryotic essential genes. Note: The sequence data for this
XX
XX CC patent did not form part of the printed specification, but was obtained
XX
XX CC in electronic format directly from WIPO at
XX
XX CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1633 AA;

Query Match 53.1%; Score 43; DB 6; Length 1633;
Best Local Similarity 61.5%; Pred. No. 3.7e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
Db 242 NDEFTQDVEYTTT 254

Search completed: August 30, 2006, 04:22:07
Job time : 55.5455 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 8.93939 Seconds
(without alignments)
161.448 Million cell updates/sec

Title: US-10-758-165A-1

Perfect score: 81

Sequence: 1 RNDSPIQDQYTTTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80.*

2: PIR1.*

3: PIR2.*

4: PIR3.*

5: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	53.1	664	2 T20420	hypothetical prote
2	42	51.9	1008	2 T32986	hypothetical prote
3	42	51.9	1067	2 D96545	probable DNA polym
4	41	50.6	1117	2 S63399	probable membrane
5	40	49.4	234	2 T49737	hypothetical prote
6	40	49.4	1157	2 F97255	fusion of alpha-gl
7	40	49.4	2094	2 S33124	tpr protein - huma
8	39	48.1	187	2 JC4806	core protein G - p
9	39	48.1	187	2 S22331	gene G protein - p
10	39	48.1	294	2 T08408	transcription fact
11	39	48.1	514	2 S72443	DNA-binding protei
12	39	48.1	564	1 HMVADA	hemagglutinin prec
13	39	48.1	587	2 F85084	probable athila-li
14	39	48.1	940	2 T01834	hypothetical prote
15	39	48.1	2161	1 A45389	genome polyprotein
16	39	48.1	26926	1 T38344	titin, cardiac mus
17	38.5	47.5	1157	1 S49247	parasporeal crystal
18	38	46.9	173	2 S55150	hypothetical prote
19	38	46.9	201	2 T31492	hypothetical prote
20	38	46.9	205	2 T31489	hypothetical prote
21	38	46.9	254	2 F81265	cysQ protein homol
22	38	46.9	281	2 AD2052	hypothetical prote
23	38	46.9	321	2 B32801	fimbrial adhesin p
24	38	46.9	335	2 JE0115	zinc-finger protei
25	38	46.9	429	2 E84410	GTP-binding protei
26	38	46.9	450	2 A10345	probable heat choc
27	38	46.9	468	2 T08139	shaggy-like protei
28	38	46.9	612	2 C90374	hypothetical prote
29	38	46.9	996	2 S76194	hypothetical prote

30 38 46.9 1158 2 AF1852 hypothetical prote
31 38 46.9 1450 2 A44027 165K myofibrillar
32 38 46.9 1465 2 S43529 165K protein, skel
33 38 46.9 1562 2 T07323 DNA-directed RNA p
34 38 46.9 1969 2 T38495 hypothetical prote
35 37.5 46.3 272 2 B69688 glutamate racemase
36 37.5 46.3 590 2 S63193 hypothetical prote
37 37 45.7 136 2 F84234 hypothetical prote
38 37 45.7 219 2 E71841 hypothetical prote
39 37 45.7 245 2 T23844 hypothetical prote
40 37 45.7 268 2 A71966 hypothetical prote
41 37 45.7 298 2 A70238 hypothetical prote
42 37 45.7 429 2 T06296 extensin-like prot
43 37 45.7 502 2 E71963 probable cardiolip
44 37 45.7 521 2 A48650 agrocarnopine utili
45 37 45.7 521 2 A13244 hypothetical prote

ALIGNMENTS

RESULT 1

T20420

hypothetical protein E02H4.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T20420

R;Barlow, K.

submitted to the EMBL Data Library, November 1995

A;Reference number: Z19273

A;Accession: T20420

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-664 <WIL>

A;Cross-references: UNIPROT:Q19038; UNIPARC:UPI0000129186; EMBL:Z68003; PIDN:CAA91975.1;

A;Experimental source: clone E02H4

C;Genetics:

A;Gene: CESP:E02H4.1

A;Map position: X

A;Introns: 57/3; 102/3; 135/3; 166/1; 191/1; 221/2; 254/3; 314/2; 355/2; 386/1; 472/3; 5

C;Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repe

Query Match 53.1%; Score 43; DB 2; Length 664;

Best Local Similarity 80.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIOTDQYTTT 14

Db 536 PCQDQYTTT 545

RESULT 2

T32986

hypothetical protein C05D2.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T32986

R;Du, Z.

submitted to the EMBL Data Library, February 1998

A;Description: The sequence of C. elegans cosmid C05D2.

A;Reference number: Z21260

A;Accession: T32986

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1008 <DUZ>

A;Cross-references: UNIPARC:UPI000017B734; EMBL:AF047651; PIDN:AA02723.1; GSPDB:GN00021

A;Experimental source: strain Bristol N2; clone C05D2

C;Genetics:

A;Gene: CESP:C05D2.6

A;Map position: 3

A;Introns: 23/1; 53/3; 141/1; 231/3; 307/3; 325/2; 420/1; 466/3; 499/3; 522/2; 594/1; 75

Query Match 51.9%; Score 42; DB 2; Length 1008;

```
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPIQTDQYT 12
   |||:|:|
Db 41 REDPPVKTQYT 52

RESULT 3
D96545
probable DNA polymerase A family protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D96545
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96545
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1067 <STO>
A;Cross-references: UNIPROT:Q9CGJ5; UNIPARC:UPI0000048370; GB:AE005173; NID:g11094700; F
C;Genetics:
A;Gene: F8A12.8
A;Map position: 1

Query Match 51.9%; Score 42; DB 2; Length 1067;
Best Local Similarity 42.9%; Pred. No. 41;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTG 15
   |||:|:|
Db 625 SDSPLSTNFVTSQ 638

RESULT 4
S63399
probable membrane protein YNR067c - Yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N3547
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63399
R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
A;Accession: S63399
A;Molecule type: DNA
A;Residues: 1-1117 <DUE>
A;Cross-references: UNIPROT:P53753; UNIPARC:UPI000013BACB; EMBL:271682; NID:g1302597; PI
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YNR067c
A;Cross-references: SGD:S0005350
A;Map position: 14R
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>

Query Match 50.6%; Score 41; DB 2; Length 1117;
Best Local Similarity 58.3%; Pred. No. 65;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTT 13
   |||:|:|
Db 430 NDGPIQTNKFT 441
```

```
RESULT 5
T49737
hypothetical protein B24B19.90 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49737
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <SCH>
A;Cross-references: UNIPARC:UPI0000179D8A; EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.90
A;Experimental source: BAC clone B24B19; strain OR74A
C;Genetics:
A;Gene: NCSP:B24B19.90
A;Map position: 6
A;Introns: 132/2
C;Superfamily: Neurospora crassa hypothetical protein B24B19.90

Query Match 49.4%; Score 40; DB 2; Length 234;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIQTDQYTTT 14
   |||:|:|
Db 65 PVPTTQYTTT 74

RESULT 6
F97255
fusion of alpha-glucosidase (family 31 glycosyl hydrolase) and glycosidase (Trea/Mals fa
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97255
R;Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97255
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1157 <KUR>
A;Cross-references: UNIPROT:Q97F62; UNIPARC:UPI000000D755C; GB:AE001437; PIDN:AAK80833.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2891

Query Match 49.4%; Score 40; DB 2; Length 1157;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTT 13
   |||:|:|
Db 889 NESDVFTQYTT 900

RESULT 7
S33124
tpr protein - human
N;Alternate names: kinase-related transforming protein (tpr-met); protein with promoter
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S33124; S23740; S00928; G01185
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2329-2333, 1992
A;Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive coi
A;Reference number: S33124; MUID:93064711; PMID:1437155
A;Accession: S33124
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
```

A;Molecule type: mRNA
A;Residues: 1-2094 <MIT>
A;Cross-references: UNIPROT:Q15624; UNIPROT:Q9UE33; UNIPARC:UPI000017CBF3; EMBL:X66397;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 383-388, 1992
A;Title: Nucleotide sequence analysis of human tpr cDNA clones.
A;Reference number: S23740; MUID:92195670; PMID:1549355
A;Accession: S23740
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-725, 'L', <MI2>
A;Cross-references: UNIPARC:UPI000062253; EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID
R;King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
Oncogene 2, 617-619, 1988
A;Title: Tpr homologues activate met and raf.
A;Reference number: S00928; MUID:88262257; PMID:3387099
A;Accession: S00928
A;Molecule type: mRNA
A;Residues: 1-31, 'R', 33-142 <KIN>
A;Cross-references: UNIPARC:UPI000016B112; EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID
R;Greco, A.
Submitted to the EMBL Data Library, December 1995
A;Reference number: H00592
A;Accession: G01185
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 144-228 <GRE>
A;Cross-references: UNIPARC:UPI00000711D7; EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; E
C;Genetics:
A;Gene: GDB:TPR
A;Cross-references: GDB:128821; OMIM:189940
A;Map position: 1q25-1q25
A;Introns: 177/3

Query Match 49.4%; Score 40; DB 2; Length 2094;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 PIQTDQVTTT 14
DB 1922 PLQSDQQT 1931
RESULT 8
JC4806
core protein G - phage phi-K
C;Species: phage phi-K
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: JC4806; B04253; A04253
R;Kodaira, K.; Oki, M.; Kakikawa, M.; Kimoto, H.; Taketo, A.
J. Biochem. 119, 1062-1069, 1996
A;Title: The virion proteins encoded by bacteriophage phi-K and its host-range mutant ph
A;Reference number: JC4804; MUID:96424987; PMID:8827438
A;Accession: JC4806
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-187 <KOD>
A;Cross-references: UNIPROT:Q38042; UNIPARC:UPI0000138658; EMBL:X60323; NID:g1478118; PI
R;Sims, J.; Capon, D.; Dressler, D.
J. Biol. Chem. 254, 12615-12628, 1979
A;Title: dnaG (primase)-dependent origins of DNA replication. Nucleotide sequences of th
A;Reference number: A92247; MUID:80049950; PMID:387790
A;Accession: B04253
A;Molecule type: DNA
A;Residues: 165-187 <SIM>
A;Cross-references: UNIPARC:UPI000009C0FB
C;Comment: This protein is one of the structural components of the bacteriophage capsid.
C;Genetics:
A;Gene: G
C;Superfamily: phage phi-X174 gene G protein
C;Keywords: capsid protein

Query Match 48.1%; Score 39; DB 2; Length 187;
Best Local Similarity 40.0%; Pred. No. 19;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 RNDSPITQDQVTTTG 15
DB 8 KHDTAIQTSRFSVTG 22
RESULT 9
S22331
gene G protein - phage alpha-3
C;Species: phage alpha-3
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: S22331; C04253; A04253
R;Kodaira, K.I.; Nakano, K.; Okada, S.; Taketo, A.
Biochim. Biophys. Acta 1130, 277-288, 1992
A;Title: Nucleotide sequence of the genome of the bacteriophage alpha3: interrelationshi
A;Reference number: S22324; MUID:92223109; PMID:1532908
A;Accession: S22331
A;Molecule type: DNA
A;Residues: 1-187 <KOD>
A;Cross-references: UNIPROT:P31281; UNIPARC:UPI0000113352; EMBL:X60322; NID:g14775; PIDN
R;Sims, J.; Capon, D.; Dressler, D.
J. Biol. Chem. 254, 12615-12628, 1979
A;Title: dnaG (primase)-dependent origins of DNA replication. Nucleotide sequences of th
A;Reference number: A92247; MUID:80049950; PMID:387790
A;Accession: C04253
A;Molecule type: DNA
A;Residues: 165-187 <SIM>
A;Cross-references: UNIPARC:UPI0000000389; GB:J02444; GB:M10725; NID:g166103; PIDN:AAA32
C;Comment: This protein is one of the structural components of the bacteriophage capsid.
C;Genetics:
A;Gene: G
C;Superfamily: phage phi-X174 gene G protein
C;Keywords: capsid protein

Query Match 48.1%; Score 39; DB 2; Length 187;
Best Local Similarity 40.0%; Pred. No. 19;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 RNDSPITQDQVTTTG 15
DB 8 KHDTAIQTSRFSVTG 22
RESULT 10
T08408
transcription factor homolog F18B3.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08408
R;Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16409
A;Accession: T08408
A;Molecule type: DNA
A;Residues: 1-294 <QUE>
A;Cross-references: UNIPROT:Q9SVL2; UNIPARC:UPI000000A322F; EMBL:AL049862; GSPDB:GNO00061;
A;Experimental source: cultivar Columbia; BAC clone F18B3
C;Genetics:
A;Gene: ATSP:F18B3.150
A;Map position: 3
A;Introns: 172/3

Query Match 48.1%; Score 39; DB 2; Length 294;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 SPIQTDQY 11
DB 201 APVQTDQY 208

RESULT 11

S72443
DNA-binding protein WRKY1 - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 31-Dec-2004
C;Accession: S72443
R;Rushon, P.J.; Tovar Torres, J.; Parniske, M.; Wernert, P.; Hahlbrock, K.; Somssich, I.
EMBO J. 15, 5690-5700, 1996
A;Title: Interaction of elicitor-induced DNA-binding proteins with elicitor response element
A;Reference number: S72443; MUID:97051827; PMID:8896462
A;Accession: S72443
A;Molecule type: mRNA
A;Residues: 1-514 <RUS>
A;Cross-references: UNIPROT:Q40827; UNIPARC:UPI000000A1PF5; EMBL:U48831; NID:gl431871; PID:
C;Superfamily: DNA-binding protein WRKY1
C;Keywords: DNA binding

Query Match 48.1%; Score 39; DB 2; Length 514;
Best Local Similarity 70.0%; Pred. No. 61;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSPIQTDQYTT 12
|:|||||:
Db 53 DSPIQNNYTT 62

RESULT 12

HMIVDA
hemagglutinin precursor - influenza A virus
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jun-2000
C;Accession: B39987; A04057; F33157
R;Nobusawa, E.; Aoyama, T.; Kato, H.; Suzuki, Y.; Tateno, Y.; Nakajima, K.
Virology 182, 475-485, 1991
A;Title: Comparison of complete amino acid sequences and receptor-binding properties among
A;Reference number: A39987; MUID:91220697; PMID:2024485
A;Accession: B39987
A;Molecule type: genomic RNA
A;Residues: 1-564 <NOB>
A;Cross-references: UNIPARC:UPI000012C4D8; GB:D90307; NID:g221309; PIDN:BAAL4337.1; PID:
A;Experimental source: strain A/duck/Alberta/60/76 [H12N5]
R;Aiz, G.M.

Proc. Natl. Acad. Sci. U.S.A. 78, 7639-7643, 1981
A;Title: Sequence relationships among the hemagglutinin genes of 12 subtypes of influenza
A;Reference number: A93902; MUID:82150925; PMID:6174976
A;Accession: A04057
A;Molecule type: genomic RNA
A;Residues: 1-38, 'L', 40-51, 'G', 53-101 <AIR>
A;Cross-references: UNIPARC:UPI0000170F31; GB:J02104; NID:g324135; PIDN:AAA43180.1; PID:
A;Experimental source: strain A/duck/Alberta/60/76 [H12]
A;Note: the signal sequence and the amino end of the HA1 chain comprise residues 1-17 and
C;Genetics:

A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-342/Product: hemagglutinin HA1 #status predicted <HA1>
F;343-564/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;27,28,140,151,152,222,302,309,496,523/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 48.1%; Score 39; DB 1; Length 564;
Best Local Similarity 60.0%; Pred. NO. 68;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIQTDQYTTT 14
|:|||||:
Db 174 PVQTDYKNT 183

RESULT 13

UNIPARC:UPI0000172721; GB:L13195; NID:g289531; PID:g

F85084

probable athila-like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F85084
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: F85084
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-587 <STO>
A;Cross-references: UNIPROT:Q9N0T2; UNIPARC:UPI000009589; GB:NC_001268; NID:g7267490; P:
C;Genetics:

A;Gene: At4g08490
A;Map position: 4

Query Match 48.1%; Score 39; DB 2; Length 587;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DSPIQTDQYTTT 14
|:|||||:
Db 401 DTPPQTDQNPPT 412

RESULT 14

T01834
hypothetical protein T15F16.4 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01834
R;Antoniou, B.; Lee, T.
submitted to the EMBL Data Library, August 1998
A;Description: The sequence of A. thaliana T15F16.
A;Reference number: Z14443
A;Accession: T01834
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-940 <ANT>
A;Cross-references: UNIPROT:O81471; UNIPARC:UPI000009DA3B; EMBL:AF076275; NID:g3293582;
A;Experimental source: cultivar Columbia
C;Genetics:

A;Map position: 4
A;Introns: 108/1; 340/1
A;Note: T15F16.4

Query Match 48.1%; Score 39; DB 2; Length 940;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DSPIQTDQYTTT 14
|:|||||:
Db 754 DTPPQTDQNPPT 765

RESULT 15

A45389
genome polyprotein - canine distemper virus (strain Onderstepoort)
N;Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: canine distemper virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A45389
R;Sidhu, M.S.; Menonna, J.P.; Cook, S.D.; Dowling, P.C.; Udem, S.A.
Virology 193, 50-65, 1993
A;Title: Canine distemper virus L gene: sequence and comparison with related viruses.
A;Reference number: A45389; MUID:93174968; PMID:8438585
A;Accession: A45389
A;Molecule type: genomic RNA
A;Residues: 1-2161 <SID>
A;Cross-references: UNIPROT:P24658; UNIPARC:UPI0000172721; GB:L13195; NID:g289531; PID:g

C;Genetics:
A;Gene: L
C;Superfamily: parainfluenza virus RNA-directed RNA polymerase
C;Keywords: ATP; nucleotidyltransferase; RNA biosynthesis; RNA replication
Query Match 48.1%; Score 39; DB 1; Length 2161;
Best Local Similarity 63.6%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 2 NDSPQTQDQYT 12
|||
Db 1656 NDKFILDQYS 1666

Search completed: August 30, 2006, 04:30:58
Job time : 9.93939 secs

This Page Blank (uspto)

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:22:32 ; Search time 58.4848 Seconds
(without alignments)
237.245 Million cell updates/sec

Title: US-10-758-165A-1
Perfect score: 81
Sequence: 1 RNDSPQTQDQYTTTG 15

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	48	59.3	196	2	Q3KZ66_SCHJA	Q3kze6 schistosoma
2	46	56.8	363	2	Q2SB97_9GAMM	Q2sb97 habella che
3	45	55.6	585	2	Q47P1_THEFY	Q47pf1 thermobifid
4	44	54.3	558	2	Q6FJW7_CANGA	Q6fjw7 candida gla
5	43.5	53.7	515	2	Q3SN12_NITWN	Q3sn12 nitrobacter
6	43	53.1	310	2	Q3DWS5_CHLAU	Q3dws5 chloroflexu
7	43	53.1	340	2	Q4SKB2_TETNG	Q4skb2 tetraodon n
8	43	53.1	511	2	Q5HK05_STAEQ	Q5hk05 staphylococ
9	43	53.1	511	2	Q8CMU2_STAES	Q8cmu2 staphylococ
10	43	53.1	516	2	Q7RHP3_PLAYO	Q7rhp3 plasmodium
11	43	53.1	634	2	Q2VB08_9BACT	Q2vbu8 uncultured
12	43	53.1	664	1	DEL1_CAEEL	Q19038 caenorhabdi
13	43	53.1	699	2	Q819P8_9BIVA	Q819p8 corbicula f
14	43	53.1	809	2	Q4N289_THEPA	Q4n289 theileria p
15	43	53.1	5261	2	Q4UFT9_THEAN	Q4uft9 theileria a
16	42	51.9	127	2	Q3PUR9_NITHA	Q3pur9 nitrobacter
17	42	51.9	273	2	Q5WK1_NEUCR	Q5wvk1 neurospora
18	42	51.9	392	2	Q3MYA8_9DEL1	Q3mya8 syntrophoba
19	42	51.9	455	2	Q2XAG3_PSEPU	Q2xag3 pseudomonas
20	42	51.9	455	2	Q88D16_PSEPK	Q88d16 pseudomonas
21	42	51.9	459	2	Q3KIR7_PSEPF	Q3kir7 pseudomonas
22	42	51.9	515	2	Q400L8_CAEEL	Q400l8 caenorhabdi
23	42	51.9	516	2	Q45133_CAEEL	Q45133 caenorhabdi
24	42	51.9	700	2	Q24781_BACSP	Q24781 bacillus sp
25	42	51.9	1049	2	Q9W105_ARATH	Q9w105 arabidopsis
26	42	51.9	1067	2	Q9C6J5_ARATH	Q9c6j5 arabidopsis
27	42	51.9	1857	2	Q8TW75_METAC	Q8tm75 methanosaer
28	41	50.6	189	2	Q87R22_VIBPA	Q87r22 vibrio para
29	41	50.6	235	2	Q4L7X7_STAHI	Q4l7x7 staphylococ
30	41	50.6	264	2	Q4MVN6_BACCE	Q4mvn6 bacillus ce
31	41	50.6	299	2	Q6CIY1_KLUULA	Q6ciy1 kluyveromy

32	41	50.6	339	2	Q8RBP9_THETN	Q8rbp9 thermoanaer
33	41	50.6	360	2	Q8A5I8_BACTN	Q8a5i8 bacteroides
34	41	50.6	414	2	Q5TRD3_ANOGA	Q5trd3 anopheles g
35	41	50.6	429	2	Q757X1_ASHGO	Q757x1 ashbya gos
36	41	50.6	662	2	Q6FN92_CANGA	Q6fn92 candida gla
37	41	50.6	713	2	Q5QV82_IDILO	Q5qv82 idiomarina
38	41	50.6	860	2	Q6JWS3_9BACT	Q6jws3 uncultured
39	41	50.6	1117	1	ENGI_YEAST	P53753 saccharomyc
40	40	49.4	97	2	Q3RS02_RALME	Q3rs02 ralstonia m
41	40	49.4	99	2	Q60S88_CAEBR	Q60s88 caenorhabdi
42	40	49.4	213	2	Q5WCK0_BACSK	Q5wck0 bacillus cl
43	40	49.4	234	2	Q7RU43_NEUCR	Q7ru43 neurospora
44	40	49.4	236	2	Q56PA2_9MEYZ	Q56pa2 uncultured
45	40	49.4	255	2	Q54Z36_DICDI	Q54z36 dictyostei

ALIGNMENTS

RESULT 1
Q3KZE6_SCHJA
ID Q3KZE6_SCHJA PRELIMINARY; PRT; 196 AA.
AC Q3KZE6;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE SUGHG06457 protein (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigidae;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Peng Z., Chen Z.,
RA Han Z.-G.;
RT "New Perspectives on Host-parasite Interplay by Comparative
RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
RT Schistosoma japonicum";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AY809222; ABA40295.1; -; mRNA.
DR NON TER 196 196
FT NON TER 196 196
SQ SEQUENCE 196 AA; 21675 MW; C04EF1B36AFFAA87 CRC64;
Query Match 59.3%; Score 48; DB 2; Length 196;
Best Local Similarity 57.1%; Pred. No. 5.4;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 2 NDSPIQTQDQYTTTG 15
Db 131 SNSPVTQYETTGG 144
RESULT 2
Q2SB97_9GAMM
ID Q2SB97_9GAMM PRELIMINARY; PRT; 363 AA.
AC Q2SB97;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE DNA repair photolyase.
GN ORFNames=HCH 05408;
OS Habella chejuensis KCTC 2396.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Habellaceae; Habella.
OX NCBI_TaxID=349521;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RC STRAIN=KCTC 2396;
RX PubMed=16352867; DOI=10.1093/nar/gki1016;
RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA Park H.-S., Lee H.K., Oh T.K., Kim J.F.;
RT "Genomic blueprint of Haella chejuensis, a marine microbe producing
RT an algicidal agent";
RL Nucleic Acids Res. 33:7066-7073 (2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR ENBL; CP000155; ABC32077.1; -; Genomic_DNA.
KW GO; GO:0016829; F-lyase activity; IEA.
SQ SEQUENCE 363 AA; 41267 MW; 8A2619C94CC8D185 CRC64;

Query Match 56.8%; Score 46; DB 2; Length 363;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNDSPITQDQYTTTG 15
Db 339 RRDSPRLRDLTPPG 353

RESULT 3
Q47PFI_THEFY
ID Q47PFI_THEFY PRELIMINARY; PRT; 585 AA.
AC Q47PFI.
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Putative solute-binding dependent transport lipoprotein precursor.
GN OrderedLocusNames=Tfu_1633;
OS Thermobifida fusca (strain YX).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptosporangineae; Nocardiopsaceae; Thermobifida.
OK NCBI_TaxID=269800;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Di Bartolo G., Chain P., Schmutz J.,
RA Larimer F., Land M., Lykidis A., Richardson P.;
RT "Complete sequence of Thermobifida fusca YX.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR ENBL; CP000088; AA255668.1; -; Genomic_DNA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00496; SEP_bac_5; 1.
DR PRINTS; PR01415; ANKYRIN.
KW Complete proteome; Lipoprotein; Signal.
FT SIGNAL 1 31 Potential.
SQ SEQUENCE 585 AA; 64409 MW; E4E1PFC382E87931 CRC64;

Query Match 55.6%; Score 45; DB 2; Length 585;
Best Local Similarity 64.3%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NDSPITQDQYTTTG 15
Db 381 NDSPYHTDVITETG 394

RESULT 4
Q6FWJ7_CANGA
ID Q6FWJ7_CANGA PRELIMINARY; PRT; 558 AA.
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,

```

```

AC Q6FWJ7;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 18.
DE Candida glabrata strain CBS138 chromosome M complete sequence.
GN OrderedLocusNames=CAGL0M03003g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OK NCBI_TaxID=5478;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E., Barbe V.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Bleykasten C.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekaiia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR ENBL; CR380959; CAG62453.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS00850; MFS; 1.
KW Complete proteome; Membrane; Transmembrane; Transport.
SQ SEQUENCE 558 AA; 61177 MW; 05760736C3F432D CRC64;

Query Match 54.3%; Score 44; DB 2; Length 558;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NDSPITQDQYTTTG 15
Db 69 NDSPFQNPVEYFETG 82

RESULT 5
Q3SN12_NITWN
ID Q3SN12_NITWN PRELIMINARY; PRT; 515 AA.
AC Q3SN12;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocusNames=Nwi_3082; ORFNames=Nwi_3082;
OS Nitrobacter winogradskyi (strain Nb-255 / ATCC 25391).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Nitrobacter.
OK NCBI_TaxID=323098;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,

```

RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
 RA Vergez L., Schmutz J., Larimer F., Land M., Hauser L., Kyriakides N.,
 RA Lykidis A., Richardson P.;
 RT "Complete sequence of *Nitrobacter winogradskyi* NB-255.";
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: CP000115; ABA06329.1; -; Genomic DNA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0008170; F:N-methyltransferase activity; IEA.
 DR GO: GO:0006306; P:DNA methylation; IEA.
 DR InterPro: IPR002296; N12N6_mtfase.
 DR InterPro: IPR002052; N6_Mcase.
 DR PRINTS: PR00507; N12N6MTFRASE.
 DR PROSITE: PS00092; N6_MTASE; UNKNOWN 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 515 AA; 54223 MW; 4F973B39D823BE669 CRC64;
 CC -----
 CC Query Match 53.7%; Score 43.5; DB 2; Length 515;
 CC Best Local Similarity 60.0%; Pred. No. 1e+02;
 CC Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 CC -----
 QY 1 RNDSPITQDQYTTTG 15
 Db 420 RNDAPVLTD-YDTVG 433
 CC -----
 CC RESULT 6
 CC Q3DW55_CHL4U
 ID Q3DW55_CHL4U PRELIMINARY; PRT; 310 AA.
 AC Q3DW55;
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 22-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Peptidase C60, sortase A and B.
 GN ORFNames=CaurDRAFT_1873;
 OS *Chloroflexus aurantiacus* J-10-fl.
 OC Bacteria; Chloroflexi; Chloroflexales; Chloroflexaceae; Chloroflexus.
 OX NCBI_TaxID=324602;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=J-10-fl;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of *Chloroflexus*
 RT *aurantiacus* J-10-fl.";
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=J-10-fl;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer P., Land M.;
 RT "Annotation of the draft genome assembly of *Chloroflexus aurantiacus*
 RT J-10-fl.";
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=J-10-fl;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: AAAH02000045; EAO57904.1; -; Genomic DNA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0009058; P:biosynthesis; IEA.
 SQ SEQUENCE 310 AA; 33946 MW; EDB84C3A58A4E6B7 CRC64;
 CC -----
 CC Query Match 53.1%; Score 43; DB 2; Length 310;
 CC Best Local Similarity 53.3%; Pred. No. 70;
 CC Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 CC -----
 QY 1 RNDSPITQDQYTTTG 15
 Db 61 RGDSPLPAPQLTTS 75
 CC -----
 CC RESULT 7
 CC Q4SKB2_TETNG
 ID Q4SKB2_TETNG PRELIMINARY; PRT; 340 AA.
 AC Q4SKB2;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Chromosome 13 SCAF14566, whole genome shotgun sequence.
 GN ORFNames=GSTENG00016807001;
 OS *Tetraodon nigroviridis* (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 RA Nicaud S., Jaffe D., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
 RT "Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: CAAE01014566; CAF98920.1; -; Genomic DNA.
 SQ SEQUENCE 340 AA; 36745 MW; 1E282568C07674E5 CRC64;
 CC -----
 CC Query Match 53.1%; Score 43; DB 2; Length 340;
 CC Best Local Similarity 53.3%; Pred. No. 78;
 CC Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 CC -----
 QY 1 RNDSPITQDQYTTTG 15
 Db 322 RLDAPLADQNATTTG 336

```

RESULT 8
ID QSHKQ5_STAEQ PRELIMINARY; PRT; 511 AA.
AC QSHKQ5;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE 5'-nucleotide family protein.
GN OrderedLocusNames=SERP2289;
OS Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=176279;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RX Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Uitterback T.R., Lee C.,
RA Dmitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RT J. Bacteriol. 187:2426-2438(2005).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000029; AAW53170.1; -; Genomic_DNA.
DR TIGR; SERP2288; -.
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0009166; P:nucleotide catabolism; IEA.
DR InterPro; IPR008334; 5'-Nucleotidase_C.
DR InterPro; IPR006146; 5'-Nucleotidase_N.
DR InterPro; IPR004843; M:pesterase.
DR PANTHER; PTHR11575; 5_nucleotidase; 1.
DR Pfam; PF00145; Metallophos; 1.
DR PRINTS; PR01607; APYRASEFAMLY.
DR PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
DR Complete proteome; Metal-binding; Nucleotide-binding.
KW Staphylococcus epidermidis strain.
SQ SEQUENCE 511 AA; 57848 MW; F160793204D4149C CRC64;
CC -----
Query Match 53.1%; Score 43; DB 2; Length 511;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTT 13
DB 444 NDAPIQSDQIYT 455
||:||||:|
|:|:|:|:|

RESULT 10
Q7RHP3_PLAYO
ID Q7RHP3_PLAYO PRELIMINARY; PRT; 516 AA.
AC Q7RHP3;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 21-FEB-2006, entry version 15.
DE GAF domain protein.
GN ORFNames=PY03941;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=1YXNUN;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----

```

```
CC -----
DR EMBL; AABL01001174; EAA15729.1; -; Genomic_DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Complete proteome; Lyase.
SQ SEQUENCE 516 AA; 62120 MW; 8CBA858FA3C373FC CRC64;

Query Match      53.1%; Score 43; DB 2; Length 516;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPLOTDOY 11
Db 53 KNDEPVSTDRY 63

RESULT 11
Q2VBUS_9BACT PRELIMINARY; PRT; 634 AA.
AC Q2VBUS_9BACT
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE RTX toxins and related Ca2+-binding protein (Fragment).
OS uncultured Bacteroidetes bacterium 'SB12-18 P41A3'.
OC Bacteria; Bacteroidetes; environmental samples.
OX NCBI_TaxID=358068;
RN [1]
RA COTTELL M.T., YU L., KIRCHMAN D.L.;
RT "Sequence and Expression Analyses of Cytophaga-Like Hydrolases in a
RT Western Arctic Metagenomic Library and the Sargasso Sea.";
RL Appl. Environ. Microbiol. 71:8506-8513(2006).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; DQ272742; AB86523.1; -; Genomic_DNA.
FT NON TER 634
SQ SEQUENCE 634 AA; 66581 MW; 339F60245E3B994B CRC64;

Query Match      53.1%; Score 43; DB 2; Length 634;
Best Local Similarity 61.5%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
Db 498 NDAPITDQSVST 510

RESULT 12
DEL1_CABEL STANDARD; PRT; 664 AA.
AC Q19038;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 21-FEB-2006, entry version 39.
DE Degenerin del-1.
GN Names:del-1; ORFNames=E02H4.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RA NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Bristol N2;
RA Tavernarakis N., Shreffler W., Wang S.L., Driscoll M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=9089613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for

investigating biology.";
Science 282:2012-2018(1998).
-i- FUNCTION: Probable sodium channel subunit.
-i- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
-i- SIMILARITY: Belongs to the amiloride-sensitive sodium channel
family.
-----
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
-----
EMBL; U76403; AAB39735.1; -; mRNA.
EMBL; Z68003; CAA91975.1; -; Genomic_DNA.
PIR; T20420; T20420.
DR Ensembl; E02H4.1; Caenorhabditis elegans.
DR WormBase; WBGene0000952; del-1.
DR WormPep; E02H4.1; CE05547.
DR InterPro; IPR004726; Deg-1.
DR InterPro; IPR001873; Na+channel_ASC.
DR PANTHER; PTHR11690; Na+channel_ASC; 1.
DR Pfam; PF00858; ASC; 1.
DR PRINTS; PR01078; AMINACHANNEL.
DR TIGRFAMs; TIGR00867; deg-1; 1.
DR PROSITE; PS01206; ASC; 1.
KW Complete proteome; Glycoprotein; Ion transport; Ionic channel;
KW Membrane; Sodium; Sodium channel; Sodium transport; Transmembrane;
KW Transport.
FT CHAIN 1 664 Degenerin del-1.
FT TOPO_DOM 1 67 /FTID=PRO 0000181285.
FT TRANSMEM 68 88 Cytoplasmic (Potential).
FT TOPO_DOM 89 607 Potential.
FT TRANSMEM 608 628 Extracellular (Potential).
FT TOPO_DOM 629 664 Potential.
FT CARBOHYD 241 241 Cytoplasmic (Potential).
FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 394 394 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 508 508 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 562 562 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 664 AA; 75474 MW; 0D19C8EF79688F8D CRC64;

Query Match      53.1%; Score 43; DB 1; Length 664;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14
Db 536 PCQDQYTTT 545

RESULT 13
Q819P8_9BIVA PRELIMINARY; PRT; 699 AA.
AC Q819P8;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 2.
DT 07-FEB-2006, entry version 16.
DE Alpha-amylase.
GN Name=AmY;
OS Corbicula fluminea.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Corbiculoidea; Corbiculidae; Corbicula.
OX NCBI_TaxID=45949;
RN [1]
RA Da Lage J.-L., Van Wormhoudt A., Cariou M.-L.;
RT "Diversity and evolution of the alpha-amylase genes in Animals.";
RL Biologia 57:181-189(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=14704857; DOI=10.1007/s00018-003-3334-y;
RA Da Lage J.-L., Feller G., Janacek S.;
RT "Horizontal gene transfer from Eukarya to bacteria and domain
RT shuffling: the alpha-amylase model.";
```

```
RL Cell. Mol. Life Sci. 61:97-109(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Da Lage J.-L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF468016; AAQ17927.2; -; Genomic_DNA.
DR HGSP; P04745; 1SMD.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006589; Alp_ amyl_cat_sub.
DR InterPro; IPR006048; Alpha_ amyl_C.
DR InterPro; IPR006047; Alpha_ amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1_13.
DR Pfam; PF02806; Alpha-amylase; C; 2.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy; C; 1.
SQ SEQUENCE 699 AA; 76544 MW; 25D57008165B04CB CRC64;

Query Match 53.1%; Score 43; DB 2; Length 699;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPIDQDTYTTG 15
Db 241 QSNPEIKTSQITSLG 255

RESULT 14
Q4N289 THEPA
ID Q4N289 THEPA PRELIMINARY; PRT; 809 AA.
AC Q4N289;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=TP04_0468;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OC NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX PubMed=15994558; DOI=10.1126/science.1110439;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Domingo A.R., Wasawo D.,
RA Crabtree J., Wortman J.R., Haas B., Anguoli S.V., Creasy T.H., Lu C.,
RA Suh B., Silva J.C., Utterback T.R., Feldblyum T.V., Ferreira M.,
RA Allen J., Nierman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes.";
RL Science 309:134-137(2005).
CC [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Anguoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Ferreira M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
```

```
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AKG01000004; EAN31820.1; -; Genomic_DNA.
DR Hypothetical protein.
SQ SEQUENCE 809 AA; 92620 MW; 58FA8368C3613471 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 809;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 NDSPIQDTQYTTG 15
Db 526 NNSPTSNSPTTGG 539

RESULT 15
Q4UFT9 THEAN
ID Q4UFT9 THEAN PRELIMINARY; PRT; 5261 AA.
AC Q4UFT9;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 03-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Sfil-subtelomeric related protein family member, putative.
GN ORFNames=TA16050;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OC NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RX PubMed=15994597; DOI=10.1258/jrsm.98.7.320;
RA Pain A., Renaud H., Berriman M., Murphy L., Yeats C.A., Weir W.,
RA Kerhornou A., Aletti M., Bishop R., Bouchier C., Cochet M.,
RA Coulson R.M.R., Cronin A., de Villiers E.P., Fraser A., Fosker N.,
RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,
RA Larke N., Lord A., Maser P., McKellar S., Mooney P., Morton F.,
RA Nene V., O'Neil S., Price C., Quail M.A., Rabinowitsch E.,
RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
RA Langsley G., Rajadream M.A., McKeever D., Shiels B., Tait A.,
RA Barrell B., Hall N.;
RT "Genome of the host-cell transforming parasite Theileria annulata
RT compared with T. parva.";
RL Science 309:131-133(2005).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR940348; CAI74027.1; -; Genomic_DNA.
DR InterPro; IPR013320; ConA_like_subgrp.
DR Pfam; PF04385; FAINT; 54.
DR Kinase; Repeat; Transferase.
SQ SEQUENCE 5261 AA; 603934 MW; 79941BB6659B78E CRC64;

Query Match 53.1%; Score 43; DB 2; Length 5261;
Best Local Similarity 53.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQDTQYTTT 14
Db 4887 NDNPETKNDYTTT 4899

Search completed: August 30, 2006, 04:29:24
Job time : 61.4848 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 14.8485 Seconds
(without alignments)
88.424 Million cell updates/sec

Title: US-10-758-165a-1

Perfect score: 81

Sequence: 1 RNDSPQTQDTQTTTG 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs,* 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /EMC_Celerra_SID33/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	108	2	US-09-281-760E-37
2	81	100.0	312	2	US-09-701-623C-2
3	81	100.0	426	1	US-08-336-583-2
4	81	100.0	426	5	PCT-US95-13795-2
5	48	59.3	431	2	US-09-479-614-14
6	48	59.3	496	2	US-09-479-614-2
7	48	59.3	496	2	US-09-479-614-29
8	41	50.6	533	2	US-09-134-001C-4053
9	40	49.4	163	2	US-09-270-767-43446
10	40	49.4	667	2	US-09-328-352-4294
11	40	49.4	1180	2	US-09-206-942-65
12	40	49.4	1180	2	US-10-193-764-61
13	40	49.4	1188	2	US-09-206-942-63
14	40	49.4	1188	2	US-10-193-764-59
15	40	49.4	2186	2	US-09-949-016-10828
16	40	49.4	2349	2	US-09-538-092-914
17	38.5	47.5	625	1	US-08-532-547-7
18	38.5	47.5	625	1	US-08-532-547-9
19	38.5	47.5	625	2	US-09-019-809-7
20	38.5	47.5	625	2	US-09-019-809-9
21	38.5	47.5	625	2	US-09-471-177-7
22	38.5	47.5	625	2	US-09-471-177-9
23	38.5	47.5	1156	2	US-09-002-285-72
24	38.5	47.5	1156	2	US-09-589-477-72
25	38.5	47.5	1156	2	US-09-661-322A-28
26	38.5	47.5	1156	2	US-10-099-285A-72

27 38.5 47.5 1157 1 US-08-532-547-5 Sequence 5, Appli
28 38.5 47.5 1157 1 US-08-379-656B-5 Sequence 5, Appli
29 38.5 47.5 1157 2 US-08-455-838-5 Sequence 5, Appli
30 38.5 47.5 1157 2 US-09-019-809-5 Sequence 5, Appli
31 38.5 47.5 1157 2 US-09-471-177-5 Sequence 5, Appli
32 38.5 47.5 1157 2 US-09-220-806-5 Sequence 5, Appli
33 38 46.9 48 2 US-09-270-767-38395 Sequence 38395, A
34 38 46.9 48 2 US-09-270-767-53612 Sequence 53612, A
35 38 46.9 131 2 US-09-949-016-9319 Sequence 9319, Ap
36 38 46.9 334 2 US-09-248-796A-19132 Sequence 19132, A
37 38 46.9 485 2 US-09-489-039A-8129 Sequence 8129, A
38 38 46.9 503 2 US-09-248-796A-15409 Sequence 15409, A
39 38 46.9 769 2 US-10-191-436A-5 Sequence 5, Appli
40 38 46.9 1155 2 US-09-710-279-1780 Sequence 1780, Ap
41 38 46.9 1742 2 US-09-386-962C-4 Sequence 4, Appli
42 38 46.9 1742 2 US-09-386-959-4 Sequence 4, Appli
43 37 45.7 139 2 US-09-634-238-335 Sequence 335, App
44 37 45.7 386 2 US-09-248-796A-21802 Sequence 21802, A
45 37 45.7 420 2 US-09-844-006A-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-281-760E-37
; Sequence 37, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (460)..(462)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (530)..(530)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (568)..(568)
; OTHER INFORMATION: "n" stands for any nucleic acid

```

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (847)..(849)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (853)..(853)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1382)..(1382)
; OTHER INFORMATION: "n" stands for any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (1832)..(1832)
; OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-37
Query Match 100.0%; Score 81; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1 RNDSP1QTDQYTTTG 15
Db 43 RNDSP1QTDQYTTTG 57

RESULT 2
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2
Query Match 100.0%; Score 81; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 4.1e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1 RNDSP1QTDQYTTTG 15
Db 255 RNDSP1QTDQYTTTG 269

RESULT 3
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.

```

```

; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2
Query Match 100.0%; Score 81; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1 RNDSP1QTDQYTTTG 15
Db 357 RNDSP1QTDQYTTTG 371

RESULT 4
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 100.0%; Score 81; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNDSPQTQDQYTTG 15
|||:|:|:|:|:|:|
Db 357 RNDSPQTQDQYTTG 371

RESULT 5
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 59.3%; Score 48; DB 2; Length 431;
Best Local Similarity 61.5%; Pred. No. 3.1;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPQTQDQYTTT 14
|||:|:|:|:|:|
Db 363 NDSPVTEQQATT 375

RESULT 6
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 59.3%; Score 48; DB 2; Length 496;
Best Local Similarity 61.5%; Pred. No. 3.6;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDSPQTQDQYTTT 14
|||:|:|:|:|:|
Db 428 NDSPVTEQQATT 440

RESULT 7
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 59.3%; Score 48; DB 2; Length 496;
Best Local Similarity 61.5%; Pred. No. 3.6;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPQTQDQYTTT 14
|||:|:|:|:|:|
Db 428 NDSPVTEQQATT 440

RESULT 8
US-09-134-001C-4053
; Sequence 4053, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4053
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4053

Query Match 50.8%; Score 41; DB 2; Length 533;
Best Local Similarity 58.3%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPQTQDQYTT 13
||:|:|:|:|:|
Db 466 NDAPQSDQIYT 477

RESULT 9
US-09-270-767-43446
; Sequence 43446, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

```
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43446
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43446

Query Match      49.4%; Score 40; DB 2; Length 163;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTT 14
   ||: ||: ||: ||: ||
Db 85 RNNEPLIADNYITT 98

RESULT 10
US-09-328-352-4294
; Sequence 4294, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4294
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4294

Query Match      49.4%; Score 40; DB 2; Length 667;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIQTQDQYTTT 14
   ||: ||: ||: ||: ||
Db 614 PLEADQYTTET 623

RESULT 11
US-09-206-942-65
; Sequence 65, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-65

Query Match      49.4%; Score 40; DB 2; Length 667;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIQTQDQYTTT 14
   ||: ||: ||: ||: ||
Db 614 PLEADQYTTET 623
```

```
Query Match      49.4%; Score 40; DB 2; Length 1180;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
   ||: ||: ||: ||: ||
Db 13 RSDTNLENEYTG TG 27

RESULT 12
US-10-193-764-61
; Sequence 61, Application US/10193764
; Patent No. 6849447
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
; FILE REFERENCE: 1038-1239MIS
; CURRENT APPLICATION NUMBER: US/10/193,764
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 09/167,568
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-61

Query Match      49.4%; Score 40; DB 2; Length 1180;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
   ||: ||: ||: ||: ||
Db 13 RSDTNLENEYTG TG 27

RESULT 13
US-09-206-942-63
; Sequence 63, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-63

Query Match      49.4%; Score 40; DB 2; Length 1188;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
   ||: ||: ||: ||: ||
Db 21 RSDTNLENEYTG TG 35
```

RESULT 14
US-10-193-764-59
; Sequence 59, Application US/10193764
; Patent No. 6849447
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
; TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
; FILE REFERENCE: 1038-1239MIS
; CURRENT APPLICATION NUMBER: US/10/193,764
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 09/167,568
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 59
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-59

Query Match 49.4%; Score 40; DB 2; Length 1188;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPITQDQYTTTG 15
Db 21 RSDTNLENEYTG 35
|:|:|:|:|:|:|

RESULT 15
US-09-949-016-10828
; Sequence 10828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10828
; LENGTH: 2186
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10828

Query Match 49.4%; Score 40; DB 2; Length 2186;
Best Local Similarity 70.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14
Db 1759 PLQSDQYTTT 1768
|:|:|:|:|:|:|

Search completed: August 30, 2006, 04:33:04
Job time : 15.8485 secs

This Page Blank (uspto)

November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications_databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_NA_Main) and **.rapbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 75.7576 Seconds
(without alignments)
91.717 Million cell updates/sec

Title: US-10-758-165a-1
Perfect score: 81
Sequence: 1 RNDSPQTQDTTGTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main.*
1: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	81	100.0	15	US-10-758-165-1	Sequence 1, Appli
2	81	100.0	312	US-10-723-207-2	Sequence 2, Appli
3	81	100.0	426	US-10-214-524-28	Sequence 28, Appl
4	53	65.4	15	US-10-758-165-7	Sequence 7, Appli
5	53	65.4	567	US-10-214-524-33	Sequence 33, Appl
6	48	59.3	15	US-10-758-165-2	Sequence 2, Appli
7	48	59.3	431	US-09-479-614-14	Sequence 14, Appl
8	48	59.3	431	US-10-409-772-14	Sequence 14, Appl
9	48	59.3	496	US-09-479-614-2	Sequence 2, Appli
10	48	59.3	496	US-09-479-614-29	Sequence 29, Appl
11	48	59.3	496	US-10-214-524-25	Sequence 25, Appl
12	48	59.3	496	US-10-409-772-2	Sequence 2, Appli
13	48	59.3	496	US-10-409-772-29	Sequence 29, Appl
14	43	53.1	68	US-10-424-599-250413	Sequence 250413,
15	43	53.1	1633	US-10-282-122A-70437	Sequence 70437, A
16	42	51.9	123	US-10-437-963-169489	Sequence 169489,
17	42	51.9	161	US-10-425-115-238239	Sequence 238239,
18	41	50.6	15	US-10-758-165-3	Sequence 3, Appli
19	41	50.6	68	US-10-424-599-211575	Sequence 211575,
20	41	50.6	191	US-10-767-701-39191	Sequence 39191, A
21	41	50.6	424	US-10-451-078-2	Sequence 2, Appli
22	41	50.6	424	US-10-451-078-4	Sequence 4, Appli
23	41	50.6	513	US-10-424-599-177658	Sequence 177658,
24	41	50.6	534	US-10-724-972A-5049	Sequence 5049, Ap
25	41	50.6	569	US-10-214-524-30	Sequence 30, Appl
26	40	49.4	356	US-11-097-143-19689	Sequence 19689, A
27	40	49.4	374	US-10-732-923-17586	Sequence 17586, A

Sequence 17624, A
Sequence 355337, A
Sequence 65347, A
Sequence 135296,
Sequence 4, Appli
Sequence 4, Appli
Sequence 44580, A
Sequence 20346, A
Sequence 50637, A
Sequence 59, Appl
Sequence 26, Appl
Sequence 117513,
Sequence 145953,

ALIGNMENTS

RESULT 1

US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDTTGTG 15
| | | | | | | | | | | | | | |
Db 1 RNDSPQTQDTTGTG 15

RESULT 2

US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 2

```
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2

Query Match      100.0%; Score 81; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RNDSP1QTDQYTTTG 15
      |||||
Db      255 RNDSP1QTDQYTTTG 269
      |||||

RESULT 3
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match      100.0%; Score 81; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RNDSP1QTDQYTTTG 15
      |||||
Db      357 RNDSP1QTDQYTTTG 371
      |||||

RESULT 4
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match      100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 57.1%; Pred. No. 0.039;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RNDSP1QTDQYTTT 14
      |||:|:|:|
Db      1 RNDAPVQADRHSTT 14
      |||:|:|:|

Query Match      65.4%; Score 53; DB 5; Length 15;
Best Local Similarity 57.1%; Pred. No. 0.039;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RNDSP1QTDQYTTT 14
      |||:|:|:|
Db      1 RNDAPVQADRHSTT 14
      |||:|:|:|

RESULT 5
US-10-214-524-33
; Sequence 33, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Pig (Sus scrofa)
US-10-214-524-33

Query Match      65.4%; Score 53; DB 4; Length 567;
Best Local Similarity 57.1%; Pred. No. 2.1;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RNDSP1QTDQYTTT 14
      |||:|:|:|
Db      499 RNDAPVQADRHSTT 512
      |||:|:|:|

RESULT 6
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

Query Match      59.3%; Score 48; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.29;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
      |||:|:|:|
Db      2 NDSPVTEQQATT 14
      |||:|:|:|

RESULT 7
US-09-479-614-14
```

```
; Sequence 14, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match      59.3%; Score 48; DB 3; Length 431;
Best Local Similarity 61.5%; Pred. No. 12;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      363 NDSFVRTEQQATT 375

RESULT 8
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match      59.3%; Score 48; DB 4; Length 431;
Best Local Similarity 61.5%; Pred. No. 12;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      363 NDSFVRTEQQATT 375

RESULT 9
US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match      59.3%; Score 48; DB 3; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      428 NDSFVRTEQQATT 440

RESULT 10
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match      59.3%; Score 48; DB 3; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      428 NDSFVRTEQQATT 440

RESULT 11
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match      59.3%; Score 48; DB 4; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches      8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      428 NDSFVRTEQQATT 440
```

```
Db      428 NDSPVTEQQATT 440
||||:|:| ||
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250413
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(68)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_68150C.1.pep
; US-10-424-599-250413
Query Match      53.1%; Score 43; DB 4; Length 68;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      4 SPIQTDQYTTT 15
:| |||||
Db      21 TPRNTDQYTTIG 32

RESULT 15
US-10-282-122A-70437
; Sequence 70437, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70437
; LENGTH: 1633

Db      428 NDSPVTEQQATT 440
||||:|:| ||
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
; US-10-409-772-2
Query Match      59.3%; Score 48; DB 4; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPQTDQYTTT 14
||||:|:| ||
Db      428 NDSPVTEQQATT 440
||||:|:| ||

RESULT 13
US-10-409-772-29
; Sequence 29, Application US/10409772
; Publication No. US20030218565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
; US-10-409-772-29
Query Match      59.3%; Score 48; DB 4; Length 496;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 NDSPQTDQYTTT 14
||||:|:| ||
Db      428 NDSPVTEQQATT 440
||||:|:| ||

RESULT 14
US-10-424-599-250413
; Sequence 250413, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
```

```
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70437

Query Match      53.1%; Score 43; DB 4; Length 1633;
Best Local Similarity 61.5%; Pred. No. 3.7e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 NDSPIQTDQYTTT 14
Db      242 NDEPTQDVEYTTT 254
```

Search completed: August 30, 2006, 05:13:02
Job time : 75.7576 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 7.72727 Seconds
(without alignments)
133.695 Million cell updates/sec

Title: US-10-758-165a-1
Perfect score: 81
Sequence: 1 RNSPTQTDQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US09_NEW_PUB.psp:
2: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.psp:
3: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.psp:
4: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.psp:
5: /EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.psp:
6: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US10_NEW_PUB.psp:
7: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US11_NEW_PUB.psp:
8: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US60_NEW_PUB.psp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	50.6	462	6	US-10-953-349-22888
2	40	49.4	632	6	US-10-449-902-55064
3	40	49.4	661	7	US-11-330-403-15135
4	39	48.1	276	7	US-11-056-355B-36321
5	39	48.1	276	7	US-11-056-355B-103150
6	39	48.1	276	7	US-11-056-355B-114389
7	39	48.1	294	7	US-11-056-355B-36320
8	39	48.1	294	7	US-11-056-355B-103149
9	39	48.1	294	7	US-11-056-355B-114388
10	39	48.1	295	7	US-11-056-355B-36319
11	39	48.1	295	7	US-11-056-355B-103148
12	39	48.1	295	7	US-11-056-355B-114387
13	38	46.9	211	6	US-10-953-349-38543
14	38	46.9	294	6	US-10-953-349-38542
15	38	46.9	386	6	US-10-953-349-38541
16	38	46.9	1212	6	US-10-449-902-41189
17	38	46.9	1742	7	US-11-396-565-4
18	37	45.7	162	6	US-10-449-902-41668
19	37	45.7	193	6	US-10-449-902-54797
20	37	45.7	335	7	US-11-056-355B-24060
21	37	45.7	335	7	US-11-056-355B-105306
22	37	45.7	335	7	US-11-056-355B-116545
23	37	45.7	379	6	US-10-449-902-40015
24	37	45.7	559	7	US-11-056-355B-78228
25	37	45.7	564	7	US-11-056-355B-91394

26	37	45.7	564	7	US-11-056-355B-95150	Sequence 95150, A
27	37	45.7	598	7	US-11-056-355B-78227	Sequence 78227, A
28	37	45.7	603	7	US-11-056-355B-91393	Sequence 91393, A
29	37	45.7	603	7	US-11-056-355B-95149	Sequence 95149, A
30	37	45.7	609	7	US-11-056-355B-78226	Sequence 78226, A
31	37	45.7	614	7	US-11-056-355B-91392	Sequence 91392, A
32	37	45.7	614	7	US-11-056-355B-95148	Sequence 95148, A
33	37	45.7	987	7	US-11-056-355B-74127	Sequence 74127, A
34	37	45.7	1016	7	US-11-070-573-17	Sequence 16, Appl
35	37	45.7	1016	7	US-11-070-573-17	Sequence 17, Appl
36	37	45.7	1071	7	US-11-056-355B-74126	Sequence 74126, A
37	37	45.7	1160	7	US-11-056-355B-74125	Sequence 74125, A
38	37	45.7	1743	7	US-11-248-956-32	Sequence 32, Appl
39	36	44.4	140	7	US-11-056-355B-8760	Sequence 8760, Ap
40	36	44.4	174	7	US-11-056-355B-8759	Sequence 8759, Ap
41	36	44.4	189	7	US-11-174-307B-4644	Sequence 4644, Ap
42	36	44.4	191	7	US-11-056-355B-8758	Sequence 8758, Ap
43	36	44.4	252	7	US-11-056-355B-47040	Sequence 47040, A
44	36	44.4	292	6	US-10-471-571A-3346	Sequence 3346, Ap
45	36	44.4	292	7	US-11-056-355B-13017	Sequence 13017, A

ALIGNMENTS

RESULT 1
US-10-953-349-22888
; Sequence 22888, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22888
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22888

Query Match 50.6%; Score 41; DB 6; Length 462;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 5 PIQTDQYTTTG 15
Db 12 PSQTDRENTTG 22

RESULT 2
US-10-449-902-55064
; Sequence 55064, Application US/104499902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55064

; LENGTH: 632
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55064

Query Match 49.4%; Score 40; DB 6; Length 632;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDOY 11
|||:|:|:
Db 231 NDEPLQTOEY 240

RESULT 3

US-11-330-403-15135
; Sequence 15135, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15135

; LENGTH: 661

; TYPE: PRT

; ORGANISM: Bacillus cereus ATCC 14579
US-11-330-403-15135

Query Match 49.4%; Score 40; DB 7; Length 661;
Best Local Similarity 69.2%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NDSPIQTDOYTTT 14
|||:|:|:
Db 569 NDSIKVDTYTTT 581

RESULT 4

US-11-056-355B-36321
; Sequence 36321, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 36321

; LENGTH: 276

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: peptide

; LOCATION: (1)..(276)

; OTHER INFORMATION: Ceres Seq. ID no. 12321429

US-11-056-355B-36321

Query Match 48.1%; Score 39; DB 7; Length 276;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDOY 11
:|:|:|:
Db 183 APVQTDQY 190

RESULT 5

US-11-056-355B-103150
; Sequence 103150, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 103150

; LENGTH: 276

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: peptide

; LOCATION: (1)..(276)

; OTHER INFORMATION: Ceres Seq. ID no. 13612112

US-11-056-355B-103150

Query Match 48.1%; Score 39; DB 7; Length 276;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDOY 11
:|:|:|:
Db 183 APVQTDQY 190

RESULT 6

US-11-056-355B-114389
; Sequence 114389, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 114389

; LENGTH: 276

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: peptide

; LOCATION: (1)..(276)

; OTHER INFORMATION: Ceres Seq. ID no. 13612112

US-11-056-355B-114389

Query Match 48.1%; Score 39; DB 7; Length 276;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDOY 11
:|:|:|:
Db 183 APVQTDQY 190

RESULT 7

US-11-056-355B-36320
; Sequence 36320, Application US/11056355B
; Publication No. US20060150283A1

```
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 36320
; LENGTH: 294
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 12321428
US-11-056-355B-36320

Query Match      48.1%; Score 39; DB 7; Length 294;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SPIQTDQY 11
Db      201 APVQTDQY 208

RESULT 8
US-11-056-355B-103149
; Sequence 103149, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 103149
; LENGTH: 294
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 13612111
US-11-056-355B-103149

Query Match      48.1%; Score 39; DB 7; Length 294;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SPIQTDQY 11
Db      201 APVQTDQY 208

RESULT 9
US-11-056-355B-114388
; Sequence 114388, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 114388
; LENGTH: 294
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 13612111
US-11-056-355B-114388

Query Match      48.1%; Score 39; DB 7; Length 294;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SPIQTDQY 11
Db      201 APVQTDQY 208

RESULT 10
US-11-056-355B-36319
; Sequence 36319, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 36319
; LENGTH: 295
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(295)
; OTHER INFORMATION: Ceres Seq. ID no. 12321427
US-11-056-355B-36319

Query Match      48.1%; Score 39; DB 7; Length 295;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 SPIQTDQY 11
Db      202 APVQTDQY 209

RESULT 11
US-11-056-355B-103148
; Sequence 103148, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 103148
; LENGTH: 294
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 13612111
US-11-056-355B-103148

Query Match      48.1%; Score 39; DB 7; Length 294;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SPIQTDQY 11
Db      201 APVQTDQY 208

RESULT 12
US-11-056-355B-114388
; Sequence 114388, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 114388
; LENGTH: 294
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 13612111
US-11-056-355B-114388

Query Match      48.1%; Score 39; DB 7; Length 294;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SPIQTDQY 11
Db      201 APVQTDQY 208
```

; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 103148
; LENGTH: 295
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(295)
; OTHER INFORMATION: Ceres Seq. ID no. 13612110
US-11-056-355B-103148

Query Match 48.1%; Score 39; DB 7; Length 295;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11
:|:|:|:|
Db 202 APVQTDQY 209

RESULT 12

US-11-056-355B-114387
; Sequence 114387, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav

; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 114387
; LENGTH: 295
; TYPE: prt
; ORGANISM: Arabidopsis thaliana

; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(295)
; OTHER INFORMATION: Ceres Seq. ID no. 13612110
US-11-056-355B-114387

Query Match 48.1%; Score 39; DB 7; Length 295;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11
:|:|:|:|
Db 202 APVQTDQY 209

RESULT 13

US-10-953-349-38543
; Sequence 38543, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38543
; LENGTH: 211
; TYPE: PRP
; ORGANISM: Zea mays subsp. mays

US-10-953-349-38543

Query Match 46.9%; Score 38; DB 6; Length 211;
Best Local Similarity 46.7%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
:|:|:|:|:|
Db 66 RQEPPEQIDRYRTVG 80

RESULT 14

US-10-953-349-38542
; Sequence 38542, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38542
; LENGTH: 294
; TYPE: PRP
; ORGANISM: Zea mays subsp. mays

Query Match 46.9%; Score 38; DB 6; Length 294;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
:|:|:|:|:|
Db 149 RQEPPEQIDRYRTVG 163

RESULT 15

US-10-953-349-38541
; Sequence 38541, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38541
; LENGTH: 386
; TYPE: PRP
; ORGANISM: Zea mays subsp. mays

Query Match 46.9%; Score 38; DB 6; Length 386;
Best Local Similarity 46.7%; Pred. No. 47;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RNDSPQTQDQYTTTG 15
:|:|:|:|:|
Db 241 RQEPPEQIDRYRTVG 255

Search completed: August 30, 2006, 04:35:58
Job time : 7.72727 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 54.5455 Seconds
(without alignments)
125.735 Million cell updates/sec

Title: US-10-758-165a-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	85	100.0	15	8 ADR10602	Adr10602 Cat Ige e
2	85	100.0	431	8 ADG73237	Adg73237 Cat immun
3	85	100.0	496	6 ABP96580	Abp96580 Cat Ige h
4	85	100.0	496	6 ABU09338	Abu09338 Feline Ig
5	85	100.0	496	6 ABU09336	Abu09336 Feline Ig
6	85	100.0	496	8 ADG73251	Adg73251 Cat parti
7	85	100.0	496	8 ADG73225	Adg73225 Cat parti
8	48	56.5	15	8 ADR10601	Adr10601 Dog Ige e
9	48	56.5	312	3 AAY79995	Aay79995 Dog immun
10	48	56.5	417	2 AAW23067	Aaw23067 Canine Ig
11	48	56.5	426	2 AAR97753	Aar97753 Canine Ig
12	48	56.5	426	6 ABP96583	Abp96583 Dog Ige h
13	47	55.3	84	6 ABU55745	Abu55745 Tree cott
14	46	54.1	449	4 ABB60974	Abb60974 Drosophil
15	45	52.9	321	4 AAE12007	Aae12007 Streptomy
16	45	52.9	321	6 ABG73760	Abg73760 S. cattle
17	44	51.8	673	4 ABB71738	Abb71738 Drosophil
18	43	50.6	470	8 ADS27897	Ads27897 Bacterial
19	43	50.6	696	8 ADX67175	Adx67175 Plant ful
20	42	49.4	87	4 AAU55966	Aau55966 Propionib
21	42	49.4	87	6 ABM52485	Abm52485 Propionib
22	42	49.4	178	5 ABB83494	Abb83494 Human zin
23	42	49.4	178	7 ADB65732	Adb65732 Human pro

24	42	49.4	197	8 ABO60445	Abo60445 Human gen
25	42	49.4	236	6 ADA54799	Ada54799 Human pro
26	42	49.4	296	7 AAO27216	Aao27216 Human zin
27	42	49.4	349	4 AAM79729	Aam79729 Human pro
28	42	49.4	430	4 AAM78745	Aam78745 Human pro
29	42	49.4	536	9 ADY18750	Ady18750 PRO polyp
30	42	49.4	537	6 AAE33775	Aae33775 Human nuc
31	41	48.2	70	4 AAU59982	Aau59982 Propionib
32	41	48.2	70	6 ABM56501	Abm56501 Propionib
33	41	48.2	152	4 AAM18098	Aam18098 Peptide #
34	41	48.2	152	4 ABB37133	Abb37133 Peptide #
35	41	48.2	152	4 AAM30608	Aam30608 Peptide #
36	41	48.2	152	4 ABB22444	Abb22444 Protein #
37	41	48.2	152	4 AAM70271	Aam70271 Human bon
38	41	48.2	152	4 AAM57851	Aam57851 Human bra
39	41	48.2	152	4 AAM05733	Aam05733 Peptide #
40	41	48.2	349	4 AAU30476	Aau30476 Novel hum
41	41	48.2	381	9 AED71188	Aed71188 Corynebac
42	41	48.2	534	9 AED71186	Aed71186 Corynebac
43	41	48.2	647	4 AAG92695	Aag92695 C glutami
44	41	48.2	812	4 ABG19065	Abg19065 Novel hum
45	41	48.2	1194	8 ADP29882	Adp29882 Human sec

ALIGNMENTS

RESULT 1
ADR10602
ID ADR10602 standard; peptide; 15 AA.
XX
AC ADR10602;
XX
DT 21-OCT-2004 (first entry)
XX
DE Cat IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.
XX
KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW cat.
XX
OS Felis catus.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hammerberg B;
XX WPI; 2004-593545/57.
PT Novel antibody that specifically binds to mammalian IgE epitope, useful
PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IgE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
CC (I) is useful for testing an allergen reactivity of an IgE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IgE corresponding to amino acid
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the

CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC cat IgE 5.91 recognition site.
 XX
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15
 |||||
 Db 1 HNDSPVTEQQATTW 15

RESULT 2

ADG73237
 ID ADG73237 standard; protein; 431 AA.

XX AC ADG73237;

XX 11-MAR-2004 (first entry)

XX Cat immunoglobulin E (IgE) constant region.

XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
 KW immune response; IgE-mediated response; allergy; cat; constant region.
 XX
 XX Felis catus.

OS US2003216565-A1.

PN 20-NOV-2003.

XX 07-APR-2003; 2003US-00409772.

XX 07-JAN-1999; 99US-0115033P.

PR 07-JAN-2000; 2000US-00479614.

XX (MCCA/) MCCALL C.

FA (WEBE/) WEBER E.

XX McCall C, Weber E;

XX WPI; 2004-010802/01.

DR N-PSDB; ADG73236.

XX New isolated nucleic acid molecule encoding a portion of a feline IgE
 PT heavy chain protein, useful for treating and/or eliciting feline immune
 PT responses for IgE-mediated responses, such as allergies.

PS Claim 12; SEQ ID NO 14; 44pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a
 CC portion of a feline IgE heavy chain protein. The methods and compositions
 CC of the present invention are useful for eliciting feline immune responses
 CC for and/or treating IgE-mediated responses, such as allergies. This is
 CC the amino acid sequence of a cat immunoglobulin E (IgE) constant region.
 XX

SQ Sequence 431 AA;

Query Match 100.0%; Score 85; DB 8; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15
 |||||
 Db 362 HNDSPVTEQQATTW 376

RESULT 3

ABP96580

ID ABP96580 standard; protein; 496 AA.

XX AC ABP96580;

XX 28-MAY-2003 (first entry)

XX Cat IgE heavy chain amino acid sequence SEQ ID NO:25.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KW urticaria hives.

XX Felis catus.

PN W02003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IgE, by identifying peptide eliciting CTL response to IgE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.

XX Example 7; Page 145-147; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IgE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IgE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions;
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IgE, and in
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IgE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 XX

SQ Sequence 496 AA;

Query Match 100.0%; Score 85; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15


```

XX OS Felis catus.
XX PN US2003216565-A1.
XX PD 20-NOV-2003.
XX PF 07-APR-2003; 2003US-00409772.
XX PR 07-JAN-1999; 99US-0115033P.
XX PR 07-JAN-2000; 2000US-00479614.
XX PX (MCCA/) MCCALL C.
XX PA (WEBE/) WEBER E.
XX PI McCall C, Weber E;
XX DR WPI; 2004-010802/01.
XX DR N-PSDB; ADG73250.
XX PT New isolated nucleic acid molecule encoding a portion of a feline IgE
XX PT heavy chain protein, useful for treating and/or eliciting feline immune
XX PT responses for IGE-mediated responses, such as allergies.
XX PS Claim 8; SEQ ID NO 29; 44pp; English.
XX CC The invention describes an isolated nucleic acid molecule (I) encoding a
XX CC portion of a feline IgE heavy chain protein. The methods and compositions
XX CC of the present invention are useful for eliciting feline immune responses
XX CC for and/or treating IGE-mediated responses, such as allergies. This is
XX CC the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
XX CC chain.
XX SQ Sequence 496 AA;
      Query Match      100.0%; Score 85; DB 8; Length 496;
      Best Local Similarity 100.0%; Pred. No. 3e-06;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY 1 HNDSPVRTEQQATTW 15
         |||||
      DB 427 HNDSPVRTEQQATTW 441

RESULT 7
ADG73225
ID ADG73225 standard; protein; 496 AA.
XX AC ADG73225;
XX DT 11-MAR-2004 (first entry)
XX DE Cat partial immunoglobulin E (IgE) heavy chain #1.
XX KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
XX KW immune response; IGE-mediated response; allergy; cat; heavy chain.
XX OS Felis catus.
XX PN US2003216565-A1.
XX PD 20-NOV-2003.
XX PF 07-APR-2003; 2003US-00409772.
XX PR 07-JAN-1999; 99US-0115033P.
XX PR 07-JAN-2000; 2000US-00479614.
XX PX (MCCA/) MCCALL C.
XX PA (WEBE/) WEBER E.
XX PI McCall C, Weber E;
XX DR WPI; 2004-010802/01.
XX DR N-PSDB; ADG73250.
XX PT New isolated nucleic acid molecule encoding a portion of a feline IgE
XX PT heavy chain protein, useful for treating and/or eliciting feline immune
XX PT responses for IGE-mediated responses, such as allergies.
XX PS Claim 8; SEQ ID NO 29; 44pp; English.
XX CC The invention describes an isolated nucleic acid molecule (I) encoding a
XX CC portion of a feline IgE heavy chain protein. The methods and compositions
XX CC of the present invention are useful for eliciting feline immune responses
XX CC for and/or treating IGE-mediated responses, such as allergies. This is
XX CC the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
XX CC chain.
XX SQ Sequence 496 AA;
      Query Match      100.0%; Score 85; DB 8; Length 496;
      Best Local Similarity 100.0%; Pred. No. 3e-06;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY 1 HNDSPVRTEQQATTW 15
         |||||
      DB 427 HNDSPVRTEQQATTW 441

RESULT 8
ADRI0601
ID ADRI0601 standard; peptide; 15 AA.
XX AC ADRI0601;
XX DT 21-OCT-2004 (first entry)
XX DE Dog IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX OS Canis familiaris.
XX PN WO2004065936-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US003566.
XX PR 16-JAN-2003; 2003US-0440472P.
XX PX (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA Hammerberg B;
XX PI WPI; 2004-593545/57.
XX DR Novel antibody that specifically binds to mammalian IgE epitope, useful
XX DR for testing an allergen reactivity of IgE sample, detecting mammalian IgE
XX DR or treating asthma or anaphylactic shock.
XX OS Example 6; Page 9; 14pp; English.
XX PS The present invention relates to a novel monoclonal antibody (I) that
XX CC specifically binds to a mammalian IgE epitope, where the epitope is
XX CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
XX CC (I) is useful for testing an allergen reactivity of an IgE sample. The
XX CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX CC and corn allergens. The sample is a biological sample collected from a
XX CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
XX CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX CC antibodies recognise epitopes on canine IgE corresponding to amino acid
XX CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from

```

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE.
XX
SQ Sequence 15 AA;

Query Match 56.5%; Score 48; DB 8; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.24;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVRTEQQATT 14
||||:|:|
Db 2 NDSPIQTDQYTTT 14

RESULT 9
AAV79995
ID AAY79995 standard; protein; 312 AA.
XX
AC AAY79995;
XX
DT 15-MAY-2000 (first entry)
XX
DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
XX
KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS Canis sp.
XX
XX WO9967293-A1.
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-US013959.
XX
XX 20-JUN-1998; 98US-00100287.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY, Walfield AM;
XX
XX WPI; 2000-160578/14.
XX
XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy.
XX
XX Example 1; Page 66-68; 155pp; English.
XX
XX The present invention describes immunoglobulin E (IgE)-CH3 domain
XX antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
XX anti-asthmatic properties. (I) induces polyclonal antibodies specific for
XX a target effector site on the epsilon-heavy chain of IgE, and so
XX preventing triggering and activation of mast cells and basophils and
XX downregulation of IgE synthesis. Conjugates, or fusion peptides
XX containing (I) are used for active immunisation against IgE-mediated
XX allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
XX dermatitis. Nucleic acids that encode these compounds are useful for
XX recombinant production of corresponding peptides or in DNA vaccines.
XX Conjugates of (I) that include a promiscuous T helper cell epitope
XX (functional in genetically diverse subjects), in addition to a B cell
XX target epitope, have increased immunogenicity and may include cyclic
XX constraints (disulfide bridge) to stabilise conformational features and
XX maximize cross-reactivity to the natural target. They induce safe (non-
XX anaphylactogenic) antibodies. AAV79994 to AAY80084 represent amino acid
XX sequences used in the exemplification of the present invention
XX
SQ Sequence 312 AA;

Query Match 56.5%; Score 48; DB 3; Length 312;

Best Local Similarity 61.5%; Pred. No. 7.4;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVRTEQQATT 14
||||:|:|
Db 256 NDSPIQTDQYTTT 268

RESULT 10
AAW23067
ID AAW23067 standard; protein; 417 AA.
XX
AC AAW23067;
XX
DT 30-JUN-2005 (revised)
DT 16-JUN-2005 (revised)
DT 19-FEB-1998 (first entry)
XX
DE Canine IgE heavy chain constant region (exon 1-4 product).
XX
KW IgE; immunoglobulin; antibody; heavy chain constant region; allergy;
KW hypersensitivity; therapy; dog; antisense; immunomodulation.
XX
OS Canis familiaris.
XX
XX Key Location/Qualifiers
XX Misc-difference 55 /note= "encoded by ACC"
XX Misc-difference 56 /note= "encoded by TAC"
XX Misc-difference 67 /note= "encoded by GCC"
XX Misc-difference 83 /note= "encoded by NNT"
XX Misc-difference 174 /note= "encoded by GGN"
XX Misc-difference 175 /note= "encoded by NNG"
XX Misc-difference 176 /note= "encoded by TGN"
XX Misc-difference 203 /note= "encoded by TCC"
XX Misc-difference 204 /note= "encoded by GAC"
XX
XX WO9730156-A2.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US002322.
XX
XX 14-FEB-1996; 96US-00601197.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Mermer B, Harris RA, Siefring AE;
XX
XX WPI; 1997-425031/39.
XX
XX N-PSDB; AAT79278.
XX
XX Isolated canine IgE heavy chain constant region DNA - useful to develop
XX products for treatment of canine allergies and for immunomodulation in
XX dogs.
XX
XX Disclosure; Page 35-39; 59pp; English.
XX
XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE
XX heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
XX comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
XX peptides encoded by exons 1-6 can be produced in eukaryotic or
XX prokaryotic cells. Such peptides, and antibodies raised against them, are
XX used in methods to treat the manifestation of allergy in dogs, e.g. to
XX treat Type I immediate hypersensitivity, and for immunomodulation

```

CC CC Revised record issued on 30-JUN-2005 : Typo in comments
XX SQ Sequence 417 AA;

Query Match          56.5%; Score 48; DB 2; Length 417;
Best Local Similarity 61.5%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQATT 14
Db 353 NDSPIQTDQYTTT 365
||||:|:|

RESULT 11
ID AAR97753 standard; protein; 426 AA.
AC AAR97753;
XX DT 28-AUG-1996 (first entry)
XX DE Canine IgE.
XX KW IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX OS Canis familiaris.
XX PN WO9614867-A1.
XX PD 23-MAY-1996.
XX PF 03-NOV-1995; 95WO-US013795.
XX PR 09-NOV-1994; 94US-00336583.
XX PR 09-NOV-1994; 94US-00336891.
XX PA (MERI ) MERCK & CO INC.
XX PI Hollis GF, Patel MD;
XX WPI; 1996-277321/28.
XX DR N-PSDB; RAT29824.
XX New DNA encoding canine IgE and IgA - useful in vaccines, anti-sense
PT therapy, assays, drug screening, etc.
XX Claim 11; Page 29-30; 49pp; English.
XX The canine IgE amino acid sequence (AAR97753) was deduced from an
CC isolated gene (AAR29824) obt'd. from a canine liver DNA library. The
CC cloning of the IgE gene allows prodn. of large quantities of recombinant
CC IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IgE antibody generation). Fragments of IgE can be
CC used in vaccines or to prevent IgE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IgE-mediated immune
CC responses
XX SQ Sequence 426 AA;

Query Match          56.5%; Score 48; DB 2; Length 426;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQATT 14
Db 358 NDSPIQTDQYTTT 370
||||:|:|

RESULT 12
ID ABP96583 standard; protein; 426 AA.
XX SQ Sequence 426 AA;

Query Match          56.5%; Score 48; DB 6; Length 426;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQATT 14
Db 358 NDSPIQTDQYTTT 370
||||:|:|

XX AC ABP96583;
XX DT 28-MAY-2003 (first entry)
XX DE Dog IgE heavy chain amino acid sequence SEQ ID NO:28.
XX KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
XX anti-allergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
XX dermatologic; antiinflammatory; IgE-mediated condition; food allergy;
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX urticaria hives.
XX OS Canis familiaris.
XX PN WO2003015716-A2.
XX PD 27-FEB-2003.
XX PF 08-AUG-2002; 2002WO-US026986.
XX PR 13-AUG-2001; 2001US-0312120P.
XX PA (IGET-) IGE THERAPEUTICS INC.
XX PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX WPI; 2003-268242/26.
XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IgE, by identifying peptide eliciting CTL response to IgE
XX peptides naturally presented by major histocompatibility complex class I
XX protein.
XX Example 7; Page 152-154; 187pp; English.
XX The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IgE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IgE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IgE peptides, C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IgE, and in
CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IgE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX SQ Sequence 426 AA;

```

RESULT 13
ABU55745
ID ABU55745 standard; protein; 84 AA.
XX AC ABU55745;
XX DT 17-MAR-2003 (first entry)
XX DE Tree cotton growth regulating protein, GaGREP1.
XX KW ss; plant; growth regulating protein; PSK; phyto sulphokine-alpha;
XX KW transgenic; marker-assisted breeding; agriculture; horticulture.
XX OS Gossypium arboreum.
XX FN WO200283901-A2.
XX PD 24-OCT-2002.
XX PF 11-APR-2002; 2002WO-EP004035.
XX PR 12-APR-2001; 2001US-0283313P.
XX PA (CROP-) CROPEDESIGN NV.
XX PA (SAUT/) SAUTER M.
XX PI Sauter M, Lorbiecke R, Mironov V, Frankard V, Dillen W;
XX PI Lejeune P, Broekaert W;
XX XX
XX DR WPI; 2003-093023/08.
XX DR N-PSDB; ABX74222.
XX PT New isolated GREP nucleic acids and polypeptides controlling or modifying
XX PT the growth characteristics of a plant, useful for a wide application in
XX PT agricultural and horticultural practices, and in vitro plant cell and
XX PT tissue culture.
XX PS Claim 5; Fig 22; 156pp; English.
XX CC The invention relates to a new isolated nucleic acid encoding a growth
XX CC regulating protein (GREP), where the protein conforms to the GREP
XX CC signature sequence appearing as ABU55742, and the GREP proteins. Also
XX CC included are a vector comprising a GREP nucleic acid, or a vector
XX CC encoding the rice growth regulating polypeptide OsPSK (phyto sulphokine-
XX CC alpha) where the growth regulating proteins regulate growth and/or
XX CC development response in intact plants, a GREP transgenic plant, a
XX CC transgenic plant comprising the vector, seed/pollen and a harvestable
XX CC part of propagation material from the transgenic plant, a host cell
XX CC comprising the GREP nucleic acid, an antisense molecule consisting of 14-
XX CC 100 nucleotides targeted to the GREP signature nucleotide sequence
XX CC appearing as ABX74197, an anti-GREP antibody which specifically
XX CC recognises a GREP or its fragment, a method for altering growth and/or
XX CC activity of a plant or plant cell/storage organ comprising modulating the
XX CC level and/or activity of a GREP or the rice growth regulating peptide
XX CC OsPSK, a method for downregulating levels of a GREP or OsPSK gene product
XX CC or its activity (comprising administering or exposing GREP or OsPSK
XX CC antibodies or gene products to cells, tissues or organs of a plant) a
XX CC method for identifying an allele with desired features of a gene encoding
XX CC a GREP which comprises isolating alleles for a GREP and testing the
XX CC features of the allele by expression in a transgenic plant, a method for
XX CC identifying an allele of GREP and selecting an allele with desired
XX CC features which comprises the use of genes encoding GREP, or sequences
XX CC located in the genome in the neighbourhood of GREP genes, as molecular
XX CC markers for different GREP alleles and selecting specific GREP alleles by
XX CC marker-assisted breeding and a method for identifying regulatory
XX CC sequences of GREP growth regulating polypeptide genes. The methods and
XX CC compositions are for controlling or modifying the growth characteristics
XX CC of a plant or its organs and tissues, useful for a wide application in
XX CC agricultural and horticultural practices, and in vitro plant cell and
XX CC tissue culture. The present sequence is a growth regulating protein
XX CC Sequence 84 AA;
XX
Query Match 55.3%; Score 47; DB 6; Length 84;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 NDSFVRTEQQATT 14
DB 32 NDSFVKTQSOGTT 44
RESULT 14
ABB60974
ID ABB60974 standard; protein; 449 AA.
XX AC ABB60974;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 9714.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL05077.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 9714; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (AB557737-
XX CC AB572072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at fip.wipo.int/pub/published_pct_sequences
XX CC Sequence 449 AA;
XX
Query Match 54.1%; Score 46; DB 4; Length 449;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 HNDSPVRTEQQATTW 15
DB 133 HNDGFVRCPEALTW 147
RESULT 15
AAE12007
ID AAE12007 standard; protein; 321 AA.
XX

AC	AAE12007;
XX	
DT	19-DEC-2001 (first entry)
XX	
DE	Streptomyces cattleya modified isopenicillin N synthetase (IPNS).
XX	
KW	Isopenicillin N synthetase; IPNS; antibiotic; penicillin; oxygenase;
KW	non-haeme iron (II) dependent family; oxidase; mutant; mutain.
XX	
OS	Streptomyces cattleya.
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
PH	Misc-difference 211
FT	/note= "wild type Glu substituted with Arg"
XX	
PN	US6284483-B1.
XX	
PD	04-SEP-2001.
XX	
PX	06-OCT-1999; 99US-00413231.
PF	
XX	
PR	06-OCT-1999; 99US-00413231.
XX	
PA	(UNMS) UNIV MICHIGAN STATE.
XX	
PI	Dilley DR, Kadyrzhanova DK, Wang Z, Warner TW;
XX	
DR	WPI; 2001-615433/71.
XX	
PT	Method for producing antibiotics, particularly penicillin G or V,
PT	comprises employing a modified isopenicillin N synthetase, in either an
PT	organism or a cell-free system under the control of bicarbonate.
XX	
PS	Claim 2; Col 37-38; 27pp; English.
XX	
CC	The invention relates to a modified enzyme of a non-haeme iron (II)
CC	dependent family of oxygenases and oxidases which renders the enzyme
CC	dependent on bicarbonate for activity. The invention also related to a
CC	method for producing penicillin G or V comprises employing a modified
CC	enzyme, particularly isopenicillin N synthetase (IPNS), in either an
CC	organism or a cell-free system, under the control of bicarbonate. The
CC	modified enzymes are IPNS, deacetoxycephalosporin C synthetase (DAOCS)
CC	and deacetylcephalosporin C synthetase (DACS). The method is useful for
CC	producing antibiotics, particularly penicillin G or V. The method is
CC	useful for making organisms useful for making an antibiotic dependent on
CC	bicarbonate to make the antibiotic. The present sequence is Streptomyc
CC	cattleya modified isopenicillin N synthetase showing an Arg211 in place
CC	of Glu211
XX	
SQ	Sequence 321 AA;
	Query Match 52.9%; Score 45; DB 4; Length 321;
	Best Local Similarity 50.0%; Pred. No. 26;
	Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps
Qy	2 NDSPVRTEQQATTW 15
	: : : :
Db	61 NESTMTDORSTTW 74

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 8.93939 Seconds
(without alignments)
161.448 Million cell updates/sec

Title: US-10-758-165a-2

Perfect score: 85

Sequence: 1 HNDSPVRTQQATTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.* *

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	52.9	321	2 A58458	isopenicillin N sy
2	43.5	51.2	403	2 JC5171	D-galactose-bindin
3	43	50.6	375	2 S58484	gag protein - maiz
4	43	50.6	470	2 D87485	glutamyl-tRNA synt
5	42	49.4	247	2 AF2006	hypothetical prote
6	42	49.4	283	2 E49348	succinoglycan bios
7	42	49.4	319	2 A95976	glucosyltransferas
8	42	49.4	319	2 S40175	ExoW protein - Rhi
9	41	48.2	101	2 B97851	hypothetical prote
10	41	48.2	259	2 B85066	hypothetical prote
11	41	48.2	1449	2 T20181	hypothetical prote
12	41	48.2	1584	2 T20180	hypothetical prote
13	41	48.2	1586	2 T20179	hypothetical prote
14	40	47.1	151	2 AF0931	probable exported
15	40	47.1	270	2 F64050	glucosamine-6-phos
16	40	47.1	275	2 S21348	probable pol polyp
17	40	47.1	410	2 D87151	probable integral
18	40	47.1	513	2 S21976	probable RNA-direc
19	40	47.1	557	2 AB0204	methyl-accepting c
20	40	47.1	631	2 E71933	hypothetical prote
21	40	47.1	635	2 D84855	probable seed natu
22	39	45.9	88	2 A38112	hipB protein - Esc
23	39	45.9	113	2 C31769	T-cell receptor de
24	39	45.9	156	2 C82971	conserved hypothet
25	39	45.9	161	2 S04917	T-cell receptor de
26	39	45.9	166	2 S04934	T-cell receptor de
27	39	45.9	295	2 A37412	T-cell receptor de
28	39	45.9	336	2 S09532	int protein - phag
29	39	45.9	514	2 E86738	multidrug resistan

30	39	45.9	666	2 I58169	semaphorin III - m
31	39	45.9	771	2 D49423	semaphorin III pre
32	39	45.9	772	2 A49069	collapsin - chicke
33	39	45.9	772	2 I48747	semaphorin D - mou
34	38	44.7	393	2 T03313	gene 16 protein -
35	38	44.7	410	1 O4BS6M	cytochrome p450 10
36	38	44.7	437	2 A34800	Opaque-2 protein -
37	38	44.7	460	2 S06022	regulatory protein
38	38	44.7	527	2 J15089	glucuronosyltransf
39	38	44.7	528	2 JN0619	glucuronosyltransf
40	38	44.7	529	2 A42233	glucuronosyltransf
41	38	44.7	533	1 QRECM2	methyl-accepting c
42	38	44.7	533	2 C90953	methyl-accepting c
43	38	44.7	533	2 G85801	serine chemorecept
44	38	44.7	551	1 GRECS	methyl-accepting c
45	38	44.7	554	2 C91293	methyl-accepting c

ALIGNMENTS

RESULT 1

A58458

isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces cattleya

C;Species: Streptomyces.cattleya

C;Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

C;Accession: A58458

R;Wang, Y.G.; Li, R.F.

Acta Microbiol. Sin. 36, 87-92, 1996

A;Title: Cloning and sequencing the isopenicillin N synthetase (IPNS) gene from Streptom

A;Reference number: A58458

A;Accession: A58458

A;Molecule type: DNA

A;Residues: 1-321 <WAN>

A;Cross-references: UNIPROT:Q53932; UNIPARC:UPI000012D7FD

C;Superfamily: isopenicillin N synthase

C;Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase

F;49,213,269/Binding site: iron (His) #status predicted

Query Match 52.9%; Score 45; DB 2; Length 321;
Best Local Similarity 50.0%; Pred. No. 3.4;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPVRTQQATTW 15

Db 61 NESTMTDQRSTTW 74

RESULT 2

JC5171

D-galactose-binding periplasmic protein mglB-2 - syphilis spirochete

N;Alternate names: carbohydrate receptor; methylgalactoside transport galactose-binding

C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C;Accession: JC5171; D71295

R;Porcella, S.F.; Popova, T.G.; Hagman, K.E.; Penn, C.W.; Radolf, J.D.; Norgard, M.V.

Gene 177, 115-121, 1996

A;Title: A mgl-like operon in Treponema pallidum, the syphilis spirochete.

A;Reference number: JC5170; MUID:97080510; PMID:8921855

A;Accession: JC5171

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-403 <POR>

A;Cross-references: UNIPROT:Q08255; UNIPARC:UPI000012F062; GB:U48416; NID:G1230600; PIDN

R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876

A;Accession: D71295

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-403 <COL>
A;Cross-references: UNIPARC:UPI000012F062; GB:AE001242; GB:AE000520; NID:G3322976; PIDN:
A;Experimental source: strain Nichols
C;Comment: This protein is a component of an ATP-binding cassette operon involved in gal
C;Genetics:
A;Gene: mgIB; TP0684
C;Keywords: calcium binding; chemotaxis; periplasmic space; sugar transport
F;44,114,116,120,197,220/Binding site: galactose (Asn, His, Asp, Arg, Asn, Asp) #status
F;96,98,100,102,104,191/Binding site: calcium (Asp, Asn, Asp, Ile, Gly, Asp) #status pre

Query Match 51.2%; Score 43.5; DB 2; Length 403;
Best Local Similarity 55.6%; Pred. No. 8.1;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 HNDSPVVRTE---QQATTW 15
||||| : ||
Db 114 HNDSKVRTEGIRRALGTW 131

RESULT 3
S58484
gag protein - maize
C;Species: Zea mays (maize)
C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
C;Accession: S58484
R;Hu, W.; Das, O.P.; Messing, J.
Mol. Gen. Genet. 248, 471-480, 1995
A;Title: Zeon-1, a member of a new maize retrotransposon family.
A;Reference number: S58484; MUID:96004768; PMID:7565611
A;Accession: S58484
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-375 <HW>
A;Cross-references: UNIPARC:UPI000011DE94; EMBL:U11059; NID:G507844; PIDN:AAA93147.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

Query Match 50.6%; Score 43; DB 2; Length 375;
Best Local Similarity 56.7%; Pred. No. 9.2;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 SPVRTEQQATTW 15
||| : |||||
Db 61 SPLSTELQATPW 72

RESULT 4
D87485
glutamyI-tRNA synthetase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87485
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87485
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <STO>
A;Cross-references: UNIPROT:Q9A721; UNIPARC:UPI00000C7547; GB:AE005673; NID:gl3423356; E
C;Genetics:
A;Gene: CC1905
C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

Query Match 50.6%; Score 43; DB 2; Length 470;
Best Local Similarity 46.7%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATTW 15
||| : |||||
Db 274 HGDDEVFTDEQAISW 288

RESULT 5
AF2006
hypothetical protein alr1604 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2006
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.;
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2006
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <KUR>
A;Cross-references: UNIPROT:Q8YWK9; UNIPARC:UPI00000CE143; GB:BA000019; PIDN:BA877970.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1604

Query Match 49.4%; Score 42; DB 2; Length 247;
Best Local Similarity 33.3%; Pred. No. 8.8;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATTW 15
| : : : : ||
Db 13 HREAPIEIVRMGLTW 27

RESULT 6
E49348
succinoglycan biosynthesis glycosyltransferase (EC 2.4.1.-) exow [validated] - Rhizobium
C;Species: Rhizobium meliloti
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: E49348
R;Glucksman, M.A.; Reuber, T.L.; Walker, G.C.
J. Bacteriol. 175, 7033-7044, 1993
A;Title: Family of glycosyl transferases needed for the synthesis of succinoglycan by Rh
A;Reference number: A49348; MUID:94042869; PMID:8226645
A;Accession: E49348
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-283 <GLU>
A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000016FEBF; GB:L20758; NID:G393240; PIDN:
C;Genetics:
A;Gene: exow
C;Function:
A;Description: EC 2.4.1.-; succinoglycan biosynthesis glycosyltransferase [validated, MU
, exoU, and exow together are responsible for sugar addition to the lipid carrier
A;Pathway: succinoglycan biosynthesis
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 283;
Best Local Similarity 57.1%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NDSFVRTEQQATTW 15
||| : |||||
Db 232 NDSFQFLKQENTW 245

RESULT 7
A95976
glucosyltransferase protein (EC 2.4.1.-) [imported] - Sinorhizobium meliloti (strain 102
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95976
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: A95976
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000012A384; GB:AL591985; PIDN:CAC49473.1;
A;Experimental source: strain 1021, megaplasmid pSymb
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chai, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholt, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Contents: annotation
C;Genetics:
A;Gene: exoW; Smb21690
A;Genome: plasmid
C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase
C;Keywords: Glycosyltransferase; hexosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 319;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 NDSFVTEQQATTW 15
||||| :|||
Db 232 NDSFQFLKQGFNTW 245

RESULT 8
S40175
ExoW protein - Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
A;Accession: S40175
R;Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A.
submitted to the EMBL Data Library, April 1993
A;Description: Analysis of the Rhizobium meliloti genes exoU, exoV, exoW, exoT and exoI ses.
A;Reference number: S40173
A;Accession: S40175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <BEC>
A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000012A384; EMBL:Z22646; NID:G605659; PIDN:
C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 319;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 NDSFVTEQQATTW 15
||||| :|||
Db 232 NDSFQFLKQGFNTW 245

RESULT 9
B97851
hypothetical protein RC1210 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
A;Accession: B97851
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: B97851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <KUR>
A;Cross-references: UNIPROT:Q92GB3; UNIPARC:UPI000000CC02C; GB:AE006914; PIDN:AA03748.1;

C;Genetics:
A;Gene: RC1210

Query Match 48.2%; Score 41; DB 2; Length 101;
Best Local Similarity 60.0%; Pred. No. 4.9;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HNDSPVTEQ 10
||||| :|||
Db 41 HNDPDPSTQQ 50

RESULT 10
B85066
hypothetical protein AT4g05260 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85066
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85066
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <STO>
A;Cross-references: UNIPROT:Q9M0W9; UNIPARC:UPI000000A640D; GB:NC_001268; NID:G7267286; P C;Genetics:
A;Gene: AT4g05260
A;Map position: 4

Query Match 48.2%; Score 41; DB 2; Length 259;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HNDSPVTEQ 11
||||| :|||
Db 140 HQDSPVRNNEQ 150

RESULT 11
T20181
hypothetical protein C53B4.4c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
A;Accession: T20181
R;Barks, M.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19233
A;Accession: T20181
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1449 <WIL>
A;Cross-references: UNIPROT:Q9U3L2; UNIPARC:UPI00001641A7; EMBL:Z68215; PIDN:CAB54213.1;
C;Genetics:
A;Experimental source: clone C53B4
A;Gene: CBSP:C53B4.4c
A;Map position: 4
A;Introns: 15/3; 92/2; 252/3; 306/1; 477/2; 571/1; 605/1; 720/3; 880/3; 1008/2; 1091/1;

Query Match 48.2%; Score 41; DB 2; Length 1449;
Best Local Similarity 58.3%; Pred. No. 92;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSFVTEQQAT 13
||||| :|||
Db 423 NNVPFIRSEQAT 434

RESULT 12
T20180
hypothetical protein C53B4.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T20180

R;Berk, M.

submitted to the EMBL Data Library, December 1995

A;Reference number: Z19233

A;Accession: T20180

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1584 <WIL>

A;Cross-references: UNIPROT:Q18798; UNIPARC:UPI000002A219; EMBL:Z68215; PIDN:CAA92457.1;

A;Experimental source: clone C53B4

C;Genetics:

A;Gene: CESP:C53B4.4a

A;Map position: 4

A;Introns: 61/2; 150/3; 227/2; 387/3; 441/1; 612/2; 706/1; 740/1; 855/3; 1015/3; 1143/2;

C;Superfamily: Caenorhabditis elegans hypothetical protein C53B4.4c

Query Match 48.2%; Score 41; DB 2; Length 1584;

Best Local Similarity 58.3%; Pred. No. 1e+02;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NDSPVTEQQAT 13

Db 558 NNVPISRQAT 569

||:|:|:|

RESULT 13

T20179

hypothetical protein C53B4.4b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T20179

R;Berk, M.

submitted to the EMBL Data Library, December 1995

A;Reference number: Z19233

A;Accession: T20179

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1586 <WIL>

A;Cross-references: UNIPROT:Q18798; UNIPARC:UPI00000866B7; EMBL:Z68215; PIDN:CAA92456.1;

A;Experimental source: clone C53B4

C;Genetics:

A;Gene: CESP:C53B4.4b

A;Map position: 4

A;Introns: 61/2; 150/3; 227/2; 387/3; 441/1; 612/2; 706/1; 740/1; 855/3; 1015/3; 1145/2;

C;Superfamily: Caenorhabditis elegans hypothetical protein C53B4.4c

Query Match 48.2%; Score 41; DB 2; Length 1586;

Best Local Similarity 58.3%; Pred. No. 1e+02;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NDSPVTEQQAT 13

Db 558 NNVPISRQAT 569

||:|:|:|

RESULT 14

AF0931

probable exported protein [imported] - Salmonella enterica subsp. enterica serovar Typhi

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AF0931

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AF0931

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-151 <PAR>

A;Cross-references: UNIPARC:UPI000013C475; GB:AL513382; PIDN:CAD09472.1; PID:G16504589;

C;Genetics:

A;Gene: STY3713

Query Match 47.1%; Score 40; DB 2; Length 151;

Best Local Similarity 80.0%; Pred. No. 12;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SPVTEQQAT 13

Db 42 SPLTTEQQAT 51

||:|:|:|

RESULT 15

F64050

glucosamine-6-phosphate deaminase (EC 3.5.99.6) - Haemophilus influenzae (strain Rd KW20

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C;Accession: F64050

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;

Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.;

D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: F64050

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-270 <TIGR>

A;Cross-references: UNIPROT:P44538; UNIPARC:UPI0000012FD06; GB:U32700; GB:L42023; MID:g32

C;Superfamily: Glucosamine-6-phosphate isomerase

C;Keywords: hydrolase; isomerase

Query Match 47.1%; Score 40; DB 2; Length 270;

Best Local Similarity 54.5%; Pred. No. 22;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVTEQQATTW 15

Db 5 PLQTEQQVSCW 15

||:|:|:|

Search completed: August 30, 2006, 04:30:55

Job time : 10.9394 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:22:32 ; Search time 58.4848 Seconds
(without alignments)
237.245 Million cell updates/sec

Title: US-10-758-165a-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	50	58.8	397	2	Q6Q4A6 TETTH
2	50	58.8	1522	2	Q5CQB3 CRYPV
3	48	56.5	735	2	Q8XXG1 RALSO
4	47	55.3	84	2	Q7PCB5 GOSAR
5	47	55.3	1083	2	Q94189 CRYNE
6	47	55.3	2360	2	Q94188 CRYNE
7	47	55.3	2360	2	Q55R83 CRYNE
8	47	55.3	2360	2	Q5KEY7 CRYNE
9	46	54.1	425	2	Q9VG84 DROME
10	46	54.1	446	2	Q3ZAP4 DROME
11	46	54.1	449	2	Q8MTZ6 DROME
12	46	54.1	526	2	Q6AWF6 DROME
13	46	54.1	621	2	Q9VGS5 DROME
14	45.5	53.5	700	2	Q8SQK3 ENCCU
15	45	52.9	79	2	Q48E23 PSE14
16	45	52.9	296	2	Q3KEF4 PSEFP
17	45	52.9	321	1	IPNS_STRCT
18	45	52.9	407	2	Q4WHG0 ASFFU
19	44	51.8	673	2	Q9VW10 DROSOPHILA
20	43.5	51.2	403	1	MGLEB_TREPA
21	43	50.6	362	2	Q2SBJ8 HAGAMM
22	43	50.6	470	1	SYE_CAUCR
23	43	50.6	521	2	Q3W9L5 ACTO
24	43	50.6	774	2	Q8J1W9 XENLA
25	43	50.6	832	2	Q5E2F3 VIBF1
26	43	50.6	1378	2	Q4PFK4 USTMA
27	43	50.6	2742	2	Q8XX21 RALSO
28	43	50.6	2742	2	Q4SZV7 TETNG
29	42	49.4	79	2	Q4ZNL8 PSEU2
30	42	49.4	79	2	Q87WK0 PSESM
31	42	49.4	194	2	Q67J75 SYMBI

32	42	49.4	221	2	Q7PK01 ANOGA
33	42	49.4	228	2	Q4E215 TRYCR
34	42	49.4	247	2	Q8YWK9 ANASP
35	42	49.4	260	2	Q73S26 MYCPA
36	42	49.4	262	2	Q7XBD0 MAIZE
37	42	49.4	296	1	ZN75A HUMAN
38	42	49.4	319	1	EXOM_RHIME
39	42	49.4	326	2	Q6C666 YARLI
40	42	49.4	403	2	Q7Q1A0 ANOGA
41	42	49.4	646	2	Q6BGK5 PARTE
42	42	49.4	732	2	Q6LNO6 PHOPR
43	42	49.4	817	2	Q6ZPN1 MOUSE
44	42	49.4	983	2	Q4PR6 USTMA
45	42	49.4	983	2	Q96VE8 USTMA

ALIGNMENTS

RESULT 1
ID Q6Q4A6 TETTH PRELIMINARY; PRT; 397 AA.
AC Q6Q4A6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Mitogen activated protein kinase 4.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymenidae; Tetrahymena.
ON NCBI_TaxID=5911;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Arslanyolu M., Yildiz M.T.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AY560586; AAS55115.1; -; Genomic_DNA.
DR HSPP; P24941; IKE8.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 397 AA; 45764 MW; 43AEE281F714E071 CRC64;

Query Match 58.8%; Score 50; DB 2; Length 397;
Best Local Similarity 64.3%; Pred No. 5.9;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSFVTEQQATTW 15

Db 169 DDNPVTEYVATRW 182

RESULT 2

```

OSCOB3_CRYPV
ID Q5CQB3_CRYPV PRELIMINARY; PRT; 1522 AA.
AC Q5CQB3;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Possible ABC transporter with AAA domain and 12 transmembrane domains.
GN ORFNames=cgd4_1390;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RX PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
RA Lanto C.A., Deng M., Liu C., Widmer G., Tripori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum."
RL Science 304:441-445(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDA whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AAER0100009; EAK87614.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Membrane; Nucleotide-binding; Transmembrane; Transport.
KW SEQUENCE 1522 AA; 176017 MW; 75C04515093B3981 CRC64;
SQ
Query Match 58.8%; Score 50; DB 2; Length 1522;
Best Local Similarity 53.3%; Pred. No. 26;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVTRTEQQATTW 15
||| ||| ||| |||
Db 72 HNDKQVRPESEISTW 86

RESULT 3
ID Q8XXG1_RALSO PRELIMINARY; PRT; 735 AA.
AC Q8XXG1;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 21-FEB-2006, entry version 20.
DE PROBABLE BIFUNCTIONAL ENZYME : (P)PPGP SYNTHETASE II AND GUANOSINE-
DE 3',5'-BISDIPHOSPHATE 3'-PYROPHOSPHOHYDROLASE (PPGPPASE) PROTEIN
DE (EC 2.7.6.5) (EC 3.1.7.2).
GN Name=spot; OrderedLocusNames=RSC2153; ORFNames=RS01611;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangerot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

```

```

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:497-502(2002).
CC -!- FUNCTION: In eubacteria ppGpp (guanosine 3'-diphosphate 5'-
CC diphosphate) is a mediator of the stringent response that
CC coordinates a variety of cellular activities in response to
CC changes in nutritional abundance. This enzyme catalyzes the
CC formation of ppGpp which is then hydrolyzed to form ppGpp (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + GTP = AMP + guanosine 3'-diphosphate 5'-
CC triphosphate.
CC -!- PATHWAY: ppGpp metabolism; first step.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AL646068; CAD15860.1; -; Genomic DNA.
DR BioCyc; RSO1305; RSC2153-MONOMER; -.
DR GO; GO:0016597; F:amino acid binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0008893; F:guanosine-3',5'-bis(diphosphate) 3'-diphosph. .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0015969; P:guanosine tetraphosphate metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002912; ACT_bd.
DR InterPro; IPR012675; Ferredoxin_fold.
DR InterPro; IPR006674; HD_hydro.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR007685; RelA_Spot.
DR InterPro; IPR004811; Spot_rela.
DR InterPro; IPR004095; TGS.
DR InterPro; IPR012676; TGS-like.
DR Pfam; PF01842; ACT; 1.
DR Pfam; PF01966; HD; 1.
DR Pfam; PF04607; RelA_Spot; 1.
DR Pfam; PF02824; TGS; 1.
DR SMART; SM00471; HDC; 1.
DR TIGRFAMs; TIGR00691; spot_rela; 1.
KW Complete proteome; Hydrolase; Kinase; Transferase.
SQ SEQUENCE 735 AA; 81962 MW; 9A6B0054104FD241 CRC64;

Query Match 56.5%; Score 48; DB 2; Length 735;
Best Local Similarity 53.3%; Pred. No. 26;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVTRTEQQATTW 15
||| ||| ||| |||
Db 358 HHDEPDRAQQQAQHW 372

RESULT 4
Q7PCB5_GOSAR
ID Q7PCB5_GOSAR PRELIMINARY; PRT; 84 AA.
AC Q7PCB5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Putative phytosulfokine peptide precursor.
GN Name=PSK1;
OS Gossypium arboreum (Tree cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=29729;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lorbiecke R., Sauter M.M.;
RT "Comparative analysis of PSK peptide growth factor precursor

```

```
RT homologs.";
RL Plant Sci. 163:321-332 (2002).
CC -I- MISCELLANEOUS: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ third party annotation (TPA) entry.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BK000114; DA000278.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR InterPro; IPR009438; PSK.
DR Pfam; PF06404; PSK; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 84 AA; 9242 MW; 6B04F8D05EC36C9B CRC64;

Query Match 55.3%; Score 47; DB 2; Length 84;
Best Local Similarity 61.5%; Pred. No. 3.6; Indels 3; Mismatches 2; Gaps 0;
Matches 8; Conservative 0; Indels 3; Mismatches 2; Gaps 0;

QY 2 NDSPVRTEQQATT 14
   ||||| :|||
   ||||| :|||
Db 32 NDSPAKTSQGT 44

RESULT 5
O94189 CRYNE PRELIMINARY; PRT; 1083 AA.
AC O94189 CRYNE PRELIMINARY; PRT; 1083 AA.
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Phosphatidylinositol 3-kinase TOR1 (Fragment).
GN Name=TOR1;
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B3501;
RX MEDLINE=99262981; PubMed=10330150;
RA Cruz M.C., Cavallo L.M., Goriach J.M., Cox G., Perfect J.R.,
RA Cardenas M.E., Heitman J.;
RT "Rapamycin antifungal action is mediated via conserved complexes with
RT FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
RL Mol. Cell. Biol. 19:4101-4112(1999).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF098973; AAD16274.1; -; mRNA.
DR HSP; P42345; IAU.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003151; FAT.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR004003; PI3/4 kinase_cat.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR SMART; SM00146; PI3KC; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS0290; PI3_4_KINASE_3; 1.
KW Kinase; Transferase.
FT NON_TER 1083
FT NON_TER 1083
SQ SEQUENCE 1083 AA; 123973 MW; 0C48A17D758553A9 CRC64;

Query Match 55.3%; Score 47; DB 2; Length 1083;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVRTEQQATTW 15
   ||||| |||
   ||||| |||
Db 202 HADEPARQEMQRTW 216

RESULT 6
O94188 CRYNE PRELIMINARY; PRT; 2360 AA.
AC O94188 CRYNE PRELIMINARY; PRT; 2360 AA.
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Phosphatidylinositol 3-kinase TOR1.
GN Name=TOR1;
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H99;
RX MEDLINE=99262981; PubMed=10330150;
RA Cruz M.C., Cavallo L.M., Goriach J.M., Cox G., Perfect J.R.,
RA Cardenas M.E., Heitman J.;
RT "Rapamycin antifungal action is mediated via conserved complexes with
RT FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
RL Mol. Cell. Biol. 19:4101-4112(1999).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF098972; AAD16273.1; -; Genomic_DNA.
DR HSP; P42345; IAU.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity; IEA.
DR InterPro; IPR011989; ARM-like.
DR InterPro; IPR003151; FAT.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR000357; HEAT.
DR InterPro; IPR004003; PI3/4 kinase_cat.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02985; HEAT; 3.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR SMART; SM00146; PI3KC; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS0290; PI3_4_KINASE_3; 1.
KW Kinase.
SQ SEQUENCE 2360 AA; 267218 MW; ED4A1059B1AA2B2A CRC64;

Query Match 55.3%; Score 47; DB 2; Length 2360;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVRTEQQATTW 15
   ||||| |||
   ||||| |||
Db 1479 HADEPARQEMQRTW 1493

RESULT 7
Q55R83 CRYNE PRELIMINARY; PRT; 2360 AA.
AC Q55R83 CRYNE PRELIMINARY; PRT; 2360 AA.
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
```

DE Hypothetical protein.
GN ORFNames=CNBF1080;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RA "Cryptococcus neoformans serotype D sequencing,"
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AA00100030; EAL20296.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
DR InterPro; IPR011989; ARM-like.
DR InterPro; IPR000403; PI3/4_kinase_cat.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02985; HEAT; 3.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR SMART; SM00146; PI3KC; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS0290; PI3_4_KINASE_3; 1.
DR Hypothetical protein.
KW SEQUENCE 2360 AA; 267304 MW; EB7ABF966AB68ADF CRC64;
SQ
Query Match 55.3%; Score 47; DB 2; Length 2360;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 HNDSPVTEQQATTW 15
Db 1479 HADEPARQEMQRQTW 1493
RESULT 8
Q5KEY7 CRYNE PRELIMINARY; PRT; 2360 AA.
AC Q5KEY7
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, entry version 1.
DT 07-FEB-2006, sequence version 9.
DE Phosphatidylinositol 3-kinase TOR1.
GN OrderedLocustNames=CNF03740;
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JEC21;
RC PubMed=15853466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vanathavan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grenberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Perteira M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;

RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans,"
RL Science 307:1321-1324(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AE017346; AAW44029.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
DR InterPro; IPR011989; ARM-like.
DR InterPro; IPR003151; FAT.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR000357; HEAT.
DR InterPro; IPR000403; PI3/4_kinase_cat.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02985; HEAT; 3.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR SMART; SM00146; PI3KC; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS0290; PI3_4_KINASE_3; 1.
DR Complete proteome; Kinase.
KW SEQUENCE 2360 AA; 267304 MW; EB7ABF966AB68ADF CRC64;
SQ
Query Match 55.3%; Score 47; DB 2; Length 2360;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 HNDSPVTEQQATTW 15
Db 1479 HADEPARQEMQRQTW 1493
RESULT 9
Q9VGS4 DROME PRELIMINARY; PRT; 425 AA.
ID Q9VGS4 DROME
AC Q9VGS4
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 2.
DT 07-FEB-2006, entry version 19.
DE CG31299-PB, isoform B.
GN Name=nccturnin; ORFNames=Dmel CG31299;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hradek N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Furl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "*Drosophila melanogaster* release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE003690; AAF54601.2; -; Genomic_DNA.
DR FlyBase; FBgn0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 425 AA; 47584 MW; AABF2F745411D29F CRC64;

Query Match 54.1%; Score 46; DB 2; Length 425;
Best Local Similarity 53.3%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 HNDSPVTEQQATW 15
Db 109 HNDGFVRCPEALTW 123
RESULT 10
Q3ZAP4 DROME
ID Q3ZAP4 DROME PRELIMINARY; PRT; 446 AA.
AC Q3ZAP4;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE R565127P.
GN Namesnocturnin;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Celniker S.;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BT023825; AAZ86746.1; -; mRNA.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 446 AA; 49953 MW; 1F694A95A17EE6D9 CRC64;
Query Match 54.1%; Score 46; DB 2; Length 446;
Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 HNDSPVTEQQATW 15
Db 130 HNDGFVRCPEALTW 144
RESULT 11
Q8MTZ6 DROME
ID Q8MTZ6 DROME PRELIMINARY; PRT; 449 AA.
AC Q8MTZ6;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Nocturnin.
GN Namesnocturnin; ORFNames=CG31299;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730715; PubMed=11747467;
RA Dupressoir A., Morel A.-P., Barbot W., Loireau M.-P., Corbo L.,
RA Heidmann T.;
RT "Identification of four families of YCCR4- and Mg2+-dependent
RT endonuclease-related proteins in higher eukaryotes, and
RT characterization of orthologs of YCCR4 with a conserved leucine-rich
RT repeat essential for hCAFI/hPOP2 binding.";
RT BMC Genomics 2:9-9(2001).
CC -----

```
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR EMBL; AY043266; AAK85704.1; -; mRNA.
DR FlyBase; FBgn0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 449 AA; 50275 MW; 1607DF25A418A024 CRC64;

Query Match          54.1%; Score 46; DB 2; Length 449;
Best Local Similarity 53.3%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQAATW 15
    ||| ||| ||| ||| |||
Db 133 HNDGFVRCPEEALW 147

RESULT 12
O6AWF6 DROME PRELIMINARY; PRT; 526 AA.
AC O6AWF6;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE GH03334p.
GN Name=nocturnin; Synonyms=nocturnin;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Wan K., Yu C., Rubin G.M., Celniker S.;
RA Park S., Man K., Celniker S.;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR EMBL; BT015292; AAT94521.1; -; mRNA.
DR FlyBase; FBgn0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 526 AA; 58951 MW; BDE221244AB110FA CRC64;

Query Match          54.1%; Score 46; DB 2; Length 526;
Best Local Similarity 53.3%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQAATW 15
    ||| ||| ||| ||| |||
Db 210 HNDGFVRCPEEALW 224

RESULT 13
O9VGS5 DROME PRELIMINARY; PRT; 621 AA.
AC O9VGS5;
DT 01-MAY-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 2.
DT 07-FEB-2006, entry version 19.
DE CG31299-PA, isoform A.
GN Name=nocturnin; ORFName=Dmel CG31299;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Arif J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclebb J.M.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Paclebb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnick S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
```

```
[5]
RN NUCLEOTIDE SEQUENCE.
RP Berkeley Drosophila Genome Project;
RA Celnikier S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirekas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AE003690; AAF54600.2; -; Genomic_DNA.
DR FlyBase; FBGN0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 621 AA; 69511 MW; A775AD0BB776FEF1 CRC64;
Query Match 54.1%; Score 46; DB 2; Length 621;
Best Local Similarity 53.3%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATW 15
Db 305 HNDGFVRCPEALTW 319
|||||
|||||

RESULT 14
Q8SQK3 ENCCU PRELIMINARY; PRT; 700 AA.
AC Q8SQK3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 18.
DE VACUOLAR ATP SYNTHASE 95kDa SUBUNIT.
GN OrderedLocusNames=ECU09.1790;
OS Eucephalitozoon cuniculi
OC Eukaryota; Fungi; Microsporidia; Unikaryoniadae; Eucephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
Eucephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AL590451; CAD27151.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
DR GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. ; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR000711; ATPsynth_OSCP.
DR InterPro; IPR002355; Cu oxidase Cu BS.
DR InterPro; IPR002490; V_ATPase sub116.
DR PANTHER; PTHR11629; V_ATPase sub116; 1.
DR Pfam; PF01496; V_ATPase_I; 1.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 700 AA; 80782 MW; FD7D9BB62373763D CRC64;
```

```
Query Match 53.5%; Score 45.5; DB 2; Length 700;
Best Local Similarity 45.0%; Pred. No. 69;
Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

Qy 1 HNDSPVTEQQ-----ATTW 15
Db 233 HNDEAIRKQEKIRHPANTW 252
|||||
|||||

RESULT 15
Q48E23_PSE14 PRELIMINARY; PRT; 79 AA.
AC Q48E23;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocusNames=PSPPH_4249;
OS Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=264730;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;
RA Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,
RA Crabtree J., Creasy T., Daviden T.M., Haft D.H., Zafar N., Zhou L.,
RA Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,
RA Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,
RA Mansfield J., Collmer A., Buell R.;
RT "Whole-genome sequence analysis of Pseudomonas syringae pv.
phaseolicola 1448A reveals divergence among pathogens in genes
involved in virulence and transposition.";
RL J. Bacteriol. 187:6488-6498(2005).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CP000058; AAZ36295.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 79 AA; 8809 MW; D167EB243339F201 CRC64;

Query Match 52.9%; Score 45; DB 2; Length 79;
Best Local Similarity 53.3%; Pred. No. 7.7;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATW 15
Db 65 HVDTPARPEQQSTKY 79
|||||
|||||

Search completed: August 30, 2006, 04:29:16
Job time : 61.4848 secs
```

This Page Blank (uspto)

Result No.	Query			Description		
	Score	Match	Length	ID	DB	Description
1	85	100.0	431	2	US-09-479-614-14	Sequence 14, Appl
2	85	100.0	496	2	US-09-479-614-2	Sequence 2, Appli
3	85	100.0	496	2	US-09-479-614-29	Sequence 29, Appl
4	48	56.5	108	2	US-09-281-760B-37	Sequence 37, Appl
5	48	56.5	312	2	US-09-701-623C-2	Sequence 2, Appli
6	48	56.5	426	1	US-08-336-583-2	Sequence 2, Appli
7	48	56.5	426	5	PCR-US95-13795-2	Sequence 2, Appli
8	46	54.1	210	2	US-09-270-767-45299	Sequence 45299, A
9	45	52.9	321	2	US-09-413-231-8	Sequence 8, Appli
10	45	52.9	321	3	US-09-924-841-8	Sequence 43758, A
11	44	51.8	181	2	US-09-270-767-43758	Sequence 43758, A
12	42	49.4	178	2	US-10-104-047-3886	Sequence 3886, Ap
13	42	49.4	296	2	US-10-094-749-2367	Sequence 2367, Ap
14	41	48.2	381	2	US-09-605-703B-1364	Sequence 1364, Ap
15	41	48.2	534	2	US-09-605-703B-1362	Sequence 1362, Ap
16	40	47.1	540	2	US-09-949-016-8465	Sequence 8465, Ap
17	40	47.1	540	2	US-09-949-016-9052	Sequence 9052, Ap
18	39	45.9	225	2	US-09-252-991A-17094	Sequence 17094, A
19	39	45.9	655	2	US-08-556-422A-3	Sequence 3, Appli
20	39	45.9	771	1	US-08-121-713D-54	Sequence 54, Appl
21	39	45.9	771	1	US-08-835-268-54	Sequence 54, Appl
22	39	45.9	771	1	US-09-060-692-54	Sequence 54, Appl
23	39	45.9	771	2	US-08-833-391-54	Sequence 54, Appl
24	39	45.9	771	2	US-09-060-610-54	Sequence 54, Appl
25	39	45.9	771	5	PCR-US94-10151A-54	Sequence 54, Appl
26	38	44.7	127	2	US-09-270-767-39006	Sequence 39006, A

US-09-479-614-2

Query Match 100.0%; Score 85; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATTW 15

Db 427 HNDSPVRTEQQATTW 441

RESULT 3

US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 100.0%; Score 85; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATTW 15

Db 427 HNDSPVRTEQQATTW 441

RESULT 4

US-09-281-760E-37
; Sequence 37, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; EARLIER FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (451)..(451)

; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (460)..(462)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (530)..(530)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (568)..(568)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (847)..(849)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (853)..(853)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1382)..(1382)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1832)..(1832)
; OTHER INFORMATION: "n" stands for any nucleic acid
; US-09-281-760E-37

Query Match 56.5%; Score 48; DB 2; Length 108;
Best Local Similarity 61.5%; Pred. No. 0.65;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQATT 14

Db 44 NDSPVQTQDYTTT 56

RESULT 5

US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995

US-09-701-623C-2

Query Match 56.5%; Score 48; DB 2; Length 312;
Best Local Similarity 61.5%; Pred. No. 2.1;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTEQQATT 14
||||:|:|
Db 256 NDSPIQTDQVTTT 268

RESULT 6

US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336, 583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2

Query Match 56.5%; Score 48; DB 1; Length 426;
Best Local Similarity 61.5%; Pred. No. 3;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTEQQATT 14
||||:|:|
Db 358 NDSPIQTDQVTTT 370

RESULT 7

PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
; CITY: RAHWAY

; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match 56.5%; Score 48; DB 5; Length 426;
Best Local Similarity 61.5%; Pred. No. 3;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTEQQATT 14
||||:|:|
Db 358 NDSPIQTDQVTTT 370

RESULT 8

US-09-270-767-45299
; Sequence 45299, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45299
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-45299

Query Match 54.1%; Score 46; DB 2; Length 210;
Best Local Similarity 53.3%; Pred. No. 3.1;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQATTW 15
||||:|:|
Db 149 HNDGFVRCPEALTW 163

RESULT 9

US-09-413-231-8
; Sequence 8, Application US/09413231
; Patent No. 6284483
; GENERAL INFORMATION:
; APPLICANT: Dilley, David R.
; APPLICANT: Kadyrzhanova, Dina K
; ADDRESSEE: Wang, Zhenyong
; APPLICANT: Warner, Toni M

```

; TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
; TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
; FILE REFERENCE: MSU41-453
; CURRENT APPLICATION NUMBER: US/09/413,231
; CURRENT FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
; OTHER INFORMATION: from Streptomyces cattleya
; NAME/KEY: MUTAGEN
; LOCATION: (211)
; OTHER INFORMATION: Glu211 in native IPNS modified to Arg
US-09-413-231-8

Query Match          52.9%; Score 45; DB 2; Length 321;
Best Local Similarity 50.0%; Pred. No. 7.4;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      2 NDSPVTEQQATTW 15
Db      61 NESTTMDQRSTTW 74

RESULT 10
US-09-924-841-8
; Sequence 8, Application US/09924841
; Patent No. 7029888
; GENERAL INFORMATION:
; APPLICANT: Dilley, David R
; APPLICANT: Kadyrzhanova, Dina K
; APPLICANT: Wang, Zhenyong
; APPLICANT: Warner, Toni M
; TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
; TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate
; FILE REFERENCE: MSU41-453
; CURRENT APPLICATION NUMBER: US/09/924,841
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US/09/413,231
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
; OTHER INFORMATION: from Streptomyces cattleya
; NAME/KEY: MUTAGEN
; LOCATION: (211)
; OTHER INFORMATION: Glu211 in native IPNS modified to Arg
US-09-924-841-8

Query Match          52.9%; Score 45; DB 3; Length 321;
Best Local Similarity 50.0%; Pred. No. 7.4;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      2 NDSPVTEQQATTW 15
Db      61 NESTTMDQRSTTW 74

RESULT 11
US-09-270-767-43758
; Sequence 43758, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
```

```

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43758
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43758

Query Match          51.8%; Score 44; DB 2; Length 181;
Best Local Similarity 57.1%; Pred. No. 5.8;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 NDSPVTEQQATTW 15
Db      62 NCSPIQTEVQAIOIW 75

RESULT 12
US-10-104-047-3886
; Sequence 3886, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3886
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-104-047-3886

Query Match          49.4%; Score 42; DB 2; Length 178;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 HNDSPVTEQQATTW 15
Db      8 HQDFPVKKRKKLSTW 22

RESULT 13
US-10-094-749-2367
; Sequence 2367, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOUKI
```

```
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2367
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2367

Query Match 49.4%; Score 42; DB 2; Length 296;
Best Local Similarity 40.0%; Pred. No. 23;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVRTEQQATTW 15
   |||||: : : ||
Db 126 HQDFPVKKKKLSTW 140

RESULT 14
US-09-605-703B-1364
; Sequence 1364, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1364
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1364

Query Match 48.2%; Score 41; DB 2; Length 381;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 HNDSPVRTEQQATTW 15
   |||||: : : ||
Db 185 HSDKPIRHEAEKLGW 199

RESULT 15
US-09-605-703B-1362
; Sequence 1362, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
```

```
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1362
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1362

Query Match 48.2%; Score 41; DB 2; Length 534;
Best Local Similarity 40.0%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 HNDSPVRTEQQATTW 15
   |||||: : : ||
Db 185 HSDKPIRHEAEKLGW 199

Search completed: August 30, 2006, 04:33:02
Job time : 15.8485 secs
```

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 75.7576 Seconds
(without alignments)
91.717 Million cell updates/sec

Title: US-10-758-165a-2

Perfect score: 85

Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	5	US-10-758-165-2
2	85	100.0	431	3	US-09-479-614-14
3	85	100.0	431	4	US-10-409-772-14
4	85	100.0	496	3	US-09-479-614-2
5	85	100.0	496	3	US-09-479-614-29
6	85	100.0	496	4	US-10-214-524-25
7	85	100.0	496	4	US-10-409-772-2
8	85	100.0	496	4	US-10-409-772-29
9	48	56.5	15	5	US-10-758-165-1
10	48	56.5	312	5	US-10-723-207-2
11	48	56.5	426	4	US-10-214-524-28
12	47	55.3	68	4	US-10-425-115-203123
13	47	55.3	84	5	US-10-474-691-101
14	47	55.3	1083	5	US-10-732-923-13976
15	47	55.3	2360	5	US-10-732-923-13960
16	46	54.1	449	6	US-11-097-143-9714
17	45	52.9	321	3	US-09-924-841-8
18	44	51.8	194	4	US-10-437-963-145550
19	44	51.8	673	6	US-11-097-143-42006
20	43	50.6	151	4	US-10-425-115-283053
21	43	50.6	425	4	US-10-425-115-190849
22	43	50.6	433	4	US-10-425-115-189170
23	43	50.6	435	4	US-10-425-115-320857
24	43	50.6	459	4	US-10-425-115-184927
25	43	50.6	461	4	US-10-425-115-320858
26	43	50.6	470	4	US-10-369-493-16930
27	43	50.6	493	4	US-10-425-115-190842

28	43	50.6	503	4	US-10-425-115-351700	Sequence 351700,
29	43	50.6	505	4	US-10-425-115-184928	Sequence 184928,
30	43	50.6	505	4	US-10-425-115-189173	Sequence 189173,
31	43	50.6	696	4	US-10-425-114-38018	Sequence 38018, A
32	43	50.6	716	4	US-10-425-115-336115	Sequence 336115,
33	42.5	50.0	188	4	US-10-437-963-201785	Sequence 201785,
34	42	49.4	68	4	US-10-425-115-233639	Sequence 233639,
35	42	49.4	178	4	US-10-104-047-3886	Sequence 3886, Ap
36	42	49.4	178	6	US-11-072-512-3886	Sequence 3886, Ap
37	42	49.4	197	4	US-10-029-386-34079	Sequence 34079, A
38	42	49.4	262	4	US-10-425-115-220304	Sequence 220304,
39	42	49.4	296	4	US-10-094-749-2367	Sequence 2367, Ap
40	42	49.4	537	4	US-10-479-435-15	Sequence 15, Appl
41	41	48.2	152	3	US-09-864-761-37742	Sequence 37742, A
42	41	48.2	473	4	US-10-424-599-153291	Sequence 153291,
43	41	48.2	647	3	US-09-738-626-6449	Sequence 6449, Ap
44	41	48.2	671	4	US-10-767-701-45175	Sequence 45175, A
45	41	48.2	750	5	US-10-732-923-11093	Sequence 11093, A

ALIGNMENTS

RESULT 1

US-10-758-165-2

; Sequence 2, Application US/10758165

; Publication No. US20050196816A1

; GENERAL INFORMATION:

; APPLICANT: Hammerberg, Bruce

; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

; FILE REFERENCE: 5051-661

; CURRENT APPLICATION NUMBER: US/10/758,165

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: US 60/440,472

; PRIOR FILING DATE: 2003-01-16

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Felis catus

US-10-758-165-2

Query Match 100.0%; Score 85; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15

Db 1 HNDSPVTEQQATTW 15

RESULT 2

US-09-479-614-14

; Sequence 14, Application US/09479614

; Publication No. US20030013183A1

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614

; CURRENT FILING DATE: 2000-01-07

; EARLIER APPLICATION NUMBER: 60/115,033

; EARLIER FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 431

; TYPE: PRT

; ORGANISM: Felis catus

US-09-479-614-14

```
Query Match      100.0%; Score 85; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVTEQQAATTW 15
Db      362 HNDSPVTEQQAATTW 376

RESULT 3
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match      100.0%; Score 85; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVTEQQAATTW 15
Db      362 HNDSPVTEQQAATTW 376

RESULT 4
US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match      100.0%; Score 85; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVTEQQAATTW 15
Db      427 HNDSPVTEQQAATTW 441

RESULT 5
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
```

```
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match      100.0%; Score 85; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVTEQQAATTW 15
Db      427 HNDSPVTEQQAATTW 441

RESULT 6
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1-1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match      100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVTEQQAATTW 15
Db      427 HNDSPVTEQQAATTW 441

RESULT 7
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2

Query Match      100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  HNDSPVTEQQATTW 15
Db      427 HNDSPVTEQQATTW 441

RESULT 8
US-10-409-772-29
; Sequence 29, Application US/10405772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR FILING DATE: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29

Query Match      100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  HNDSPVTEQQATTW 15
Db      427 HNDSPVTEQQATTW 441

RESULT 9
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR FILING DATE: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      56.5%; Score 48; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.25;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2  NDSFVTEQQATT 14
Db      2  NDSFVTEQQATT 14

RESULT 10
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2

Query Match      56.5%; Score 48; DB 5; Length 312;
Best Local Similarity 61.5%; Pred. No. 7;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2  NDSFVTEQQATT 14
Db      256 NDSFVTEQQATT 268

RESULT 11
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match      56.5%; Score 48; DB 4; Length 426;
Best Local Similarity 61.5%; Pred. No. 9.9;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2  NDSFVTEQQATT 14
Db      256 NDSFVTEQQATT 268
```

```
Db      358 NDSPIQTDQVTTT 370

RESULT 12
US-10-425-115-203123
; Sequence 203123, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 203123
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_116836C.1.pep
US-10-425-115-203123

Query Match      55.3%; Score 47; DB 4; Length 68;
Best Local Similarity 69.2%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPIQTDQVTTT 14
      |:|||||
Db      38 NQTPVTEQQTGTT 50

RESULT 13
US-10-474-691-101
; Sequence 101, Application US/10474691
; Publication No. US20040221332A1
; GENERAL INFORMATION:
; APPLICANT: CropDesign N.V.
; TITLE OF INVENTION: Plant growth regulating genes, proteins and uses thereof
; FILE REFERENCE: CROP-028-PCT
; CURRENT APPLICATION NUMBER: US/10/474,691
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/283,313
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Gossypium arboreum
US-10-474-691-101

Query Match      55.3%; Score 47; DB 5; Length 84;
Best Local Similarity 61.5%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPIQTDQVTTT 14
      ||||:|:|
Db      32 NDSPIQTDQVTTT 44

RESULT 14
US-10-732-923-13976
; Sequence 13976, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13976
; LENGTH: 2360
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. grubii
US-10-732-923-13960

Query Match      55.3%; Score 47; DB 5; Length 2360;
Best Local Similarity 53.3%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 HNDSPIQTDQVTTT 15
      |||||
Db      1479 HADEPARQEQVTTT 1493

Search completed: August 30, 2006, 05:13:01
Job time : 76.7576 secs

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13976
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. neoformans
US-10-732-923-13976

Query Match      55.3%; Score 47; DB 5; Length 1083;
Best Local Similarity 53.3%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 HNDSPIQTDQVTTT 15
      |||||
Db      202 HADEPARQEQVTTT 216

RESULT 15
US-10-732-923-13960
; Sequence 13960, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13960
; LENGTH: 2360
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. grubii
US-10-732-923-13960

Query Match      55.3%; Score 47; DB 5; Length 2360;
Best Local Similarity 53.3%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 HNDSPIQTDQVTTT 15
      |||||
Db      1479 HADEPARQEQVTTT 1493

Search completed: August 30, 2006, 05:13:01
Job time : 76.7576 secs
```

Result No.	Score	Match	Query	Length	DB	ID	Description
1	43	50.6	980	6	US-10-449-902-41347	Sequence 41347, A	
2	39	45.9	148	6	US-10-449-902-51741	Sequence 51741, A	
3	39	45.9	771	6	US-10-505-928-255	Sequence 255, App	
4	38	44.7	151	7	US-11-330-403-4388	Sequence 4388, Ap	
5	38	44.7	153	7	US-11-330-403-5751	Sequence 5751, Ap	
6	38	44.7	156	7	US-11-330-403-4345	Sequence 4345, Ap	
7	38	44.7	174	7	US-11-330-403-7573	Sequence 7573, Ap	
8	38	44.7	242	7	US-11-330-403-12509	Sequence 12509, A	
9	38	44.7	436	6	US-10-449-902-37829	Sequence 37829, A	
10	38	44.7	527	6	US-10-196-749-522	Sequence 522, App	
11	38	44.7	530	6	US-10-700-439-165	Sequence 165, App	
12	38	44.7	596	6	US-10-519-069-18	Sequence 18, Appl	
13	38	44.7	1093	6	US-10-449-902-41297	Sequence 41297, A	
14	37.5	44.1	132	6	US-10-953-349-34917	Sequence 34917, A	
15	37.5	44.1	132	7	US-11-056-3558-7331	Sequence 7331, Ap	
16	37.5	44.1	135	6	US-10-953-349-34916	Sequence 34916, A	
17	37.5	44.1	135	7	US-11-056-3558-7330	Sequence 7330, Ap	
18	37.5	44.1	135	7	US-11-056-3558-10350	Sequence 10350, A	
19	37.5	44.1	183	6	US-10-953-349-34915	Sequence 34915, A	
20	37.5	44.1	183	7	US-11-056-3558-7329	Sequence 7329, Ap	
21	37.5	44.1	183	7	US-11-056-3558-10349	Sequence 10349, A	
22	37.5	44.1	191	6	US-10-449-902-36429	Sequence 36429, A	
23	37	43.5	115	6	US-10-953-349-256	Sequence 256, App	
24	37	43.5	115	7	US-11-056-3558-23671	Sequence 23671, A	
25	37	43.5	115	7	US-11-056-3558-104478	Sequence 104478, A	

```

; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51741
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51741

Query Match      45.9%; Score 39; DB 6; Length 148;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATW 15
   ||| ||| |||
Db 123 HNDYPLQIVQIYTPW 137

RESULT 3
US-10-505-928-255
; Sequence 255, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 255
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-255

Query Match      45.9%; Score 39; DB 6; Length 771;
Best Local Similarity 54.5%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVRTEQQATW 15
   ||| ||| |||
Db 210 PIRTEQHDSRW 220

RESULT 4
US-11-330-403-4388
; Sequence 4388, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4388
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(151)
; OTHER INFORMATION: unsure at all xaa locations
US-11-330-403-4388

Query Match      44.7%; Score 38; DB 7; Length 151;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51741
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51741

Query Match      45.9%; Score 39; DB 6; Length 148;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNDSPVRTEQQATW 15
   ||| ||| |||
Db 123 HNDYPLQIVQIYTPW 137

RESULT 3
US-10-505-928-255
; Sequence 255, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 255
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-255

Query Match      45.9%; Score 39; DB 6; Length 771;
Best Local Similarity 54.5%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVRTEQQATW 15
   ||| ||| |||
Db 210 PIRTEQHDSRW 220

RESULT 4
US-11-330-403-4388
; Sequence 4388, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4388
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(151)
; OTHER INFORMATION: unsure at all xaa locations
US-11-330-403-4388

Query Match      44.7%; Score 38; DB 7; Length 151;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 2 NDSPVRTEQQA 12
   ||| ||| ||| |||
Db 54 NDPVVRNSQEA 64

RESULT 5
US-11-330-403-5751
; Sequence 5751, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 5751
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(153)
; OTHER INFORMATION: unsure at all xaa locations
US-11-330-403-5751

Query Match      44.7%; Score 38; DB 7; Length 153;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQA 12
   ||| ||| ||| |||
Db 55 NDPVVRNSQEA 65

RESULT 6
US-11-330-403-4345
; Sequence 4345, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4345
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-4345

Query Match      44.7%; Score 38; DB 7; Length 156;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPVRTEQQA 12
   ||| ||| ||| |||
Db 57 NDPVVRNSQEA 67

RESULT 7
US-11-330-403-7573
; Sequence 7573, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250

```

US-10-449-902-37829

GENERAL INFORMATION:

; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Burgess, Christopher
; APPLICANT: Myerow, Susan
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Maimonis, Peter
; APPLICANT: Molino, Gary
; APPLICANT: Burgart, Lawrence
; APPLICANT: Boardman, Lisa A.
; APPLICANT: Thibodeau, Steven
; APPLICANT: Lewis, Marcia
; TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
; TITLE OF INVENTION: Biomarkers for Cancer
; FILE REFERENCE: 1657/2022
; CURRENT APPLICATION NUMBER: US/10/700,439
; CURRENT FILING DATE: 2003-11-04
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-439-165

Query Match 44.7%; Score 38; DB 6; Length 530;
Best Local Similarity 40.0%; Pred. No. 98;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATTW 15
|:|:|:|:|:
Db 450 HHDQVFKPLDRAVFW 464

RESULT 12
US-10-519-069-18
; Sequence 18, Application US/10519069
; Publication No. US20060121561A1
; GENERAL INFORMATION:
; APPLICANT: Fritsch Olivier
; APPLICANT: Hohn Barbara
; APPLICANT: Lucht Jan Martin
; TITLE OF INVENTION: GENE FOR INCREASED SOMATIC RECOMBINATION
; FILE REFERENCE: 1-32546B/FMI
; CURRENT APPLICATION NUMBER: US/10/519,069
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/EP03/006757
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: GB 0214896
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-519-069-18

Query Match 44.7%; Score 38; DB 6; Length 596;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PVRTEQQATTW 15
|:|:|:|:|:
Db 535 PSRTEPQFVTW 545

RESULT 13
US-10-449-902-41297
; Sequence 41297, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41297
; LENGTH: 1093
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41297

Query Match 44.7%; Score 38; DB 6; Length 1093;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQATT 14
|:|:|:|:|:
Db 98 HRESGSRPPQATS 111

RESULT 14
US-10-953-349-34917
; Sequence 34917, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34917
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34917

Query Match 44.1%; Score 37.5; DB 6; Length 132;
Best Local Similarity 53.3%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 HNDSPVTEQQATTW 15
|:|:|:|:|:
Db 101 NNDSPLENT-QAAALW 114

RESULT 15
US-11-056-355B-7331
; Sequence 7331, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 7331
; LENGTH: 132
; TYPE: prt

; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(132)
; OTHER INFORMATION: Ceres Seq. ID no. 13498699
US-11-056-355B-7331

Query Match 44.1%; Score 37.5; DB 7; Length 132;
Best Local Similarity 53.3%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 HNDSPVRTEQQATTW 15
:||||:| | | | |
Db 101 NNDSPINT-QAALW 114

Search completed: August 30, 2006, 04:35:57
Job time : 7.72727 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 54.5455 Seconds
(without alignments)
125.735 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLQTDQQAATR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	8 ADR10603	Adr10603 Horse Ige
2	74	100.0	424	5 AAM50103	Aam50103 Equine Ige
3	74	100.0	424	5 AAM50104	Aam50104 Equine Ige
4	74	100.0	566	9 AED15438	Aed15438 Equine Pr
5	74	100.0	566	10 AEE88000	Aee88000 Human pro
6	74	100.0	569	6 ABP96585	Abp96585 Horse Ige
7	49	66.2	15	7 ADC64568	Adc64568 Horse imm
8	43	58.1	417	9 AEB39722	Aeb39722 L. pneumo
9	43	58.1	452	9 AEB36305	Aeb36305 L. pneumo
10	43	58.1	580	5 ABG32001	Abg32001 Q. intest
11	43	58.1	580	8 ADP79623	Adp79623 Giardia i
12	41	55.4	312	3 AAY79995	Aay79995 Dog Ige e
13	41	55.4	312	8 ADR10601	Adr10601 Dog Ige e
14	41	55.4	312	8 ADN24060	Adn24060 Bacterial
15	41	55.4	417	2 AAW23067	Aaw23067 Canine Ige
16	41	55.4	426	2 AAR97753	Aar97753 Canine Ige
17	41	55.4	426	6 ABP96583	Abp96583 Dog Ige h
18	41	55.4	2000	6 ABR52669	Abr52669 Protein s
19	41	55.4	2000	7 ADK61774	Adk61774 Disease t
20	40	54.1	15	8 ADR10607	Adr10607 Pig Ige e
21	40	54.1	567	6 ABP96588	Abp96588 Pig Ige h
22	38	51.4	613	2 AAW73009	Aaw73009 Cobra ven
23	38	51.4	621	2 AAW73013	Aaw73013 Cobra ven

24	38	51.4	703	6 ABU44458	Abu44458 Protein e
25	38	51.4	814	6 ABJ26042	Abj26042 Aspergill
26	38	51.4	1827	9 AEC10425	Aec10425 Glycoside
27	37	50.0	15	8 ADR10602	Adr10602 Cat Ige e
28	37	50.0	66	4 AAU62291	Aau62291 Propionib
29	37	50.0	66	6 ABM58810	Abm58810 Propionib
30	37	50.0	223	8 ADJ48583	Adj48583 Oil-assoc
31	37	50.0	285	2 AAY17498	Aay17498 Zoota prot
32	37	50.0	370	6 ADA34539	Ada34539 Acinetoba
33	37	50.0	431	8 ADG73237	Adg73237 Cat immun
34	37	50.0	496	6 ABP96580	Abp96580 Cat Ige h
35	37	50.0	496	6 ABU09338	Abu09338 Feline Ige
36	37	50.0	496	6 ABU09336	Abu09336 Feline Ige
37	37	50.0	496	8 ADG73251	Adg73251 Cat parti
38	37	50.0	496	8 ADG73225	Adg73225 Cat parti
39	37	50.0	663	8 ADJ49049	Adj49049 Oil-assoc
40	37	50.0	1320	4 AAU48101	Aau48101 Propionib
41	37	50.0	1320	6 ABM44620	Abm44620 Propionib
42	36	48.6	21	7 ADM66490	Adm66490 Peptide f
43	36	48.6	75	8 ADV87747	Adv87747 Streptoco
44	36	48.6	75	8 ADV79000	Adv79000 Streptoco
45	36	48.6	143	6 ABJ26246	Abj26246 Aspergill

ALIGNMENTS

RESULT 1
ADR10603
ID ADR10603 standard; peptide; 15.AA.
XX
AC ADR10603;
XX
DT 21-Oct-2004 (first entry)
XX
DE Horse Ige epitope recognised by monoclonal antibody 5.91, SEQ ID 3.
XX
KW Antiasthmatic; Antiallergic; Immunosuppressive; Ige; dog; asthma;
anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
horse.
XX
OS Equus caballus.
XX
FN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
(UYN-) UNIV NORTH CAROLINA STATE.
XX
Hammerberg B;
XX
WPI; 2004-593545/57.
XX
Novel antibody that specifically binds to mammalian Ige epitope, useful
for testing an allergen reactivity of Ige sample, detecting mammalian Ige
or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian Ige epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige. (I) is useful for testing an allergen reactivity of an Ige sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian Ige and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine Ige corresponding to amino acid residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the

CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC horse IgE 5.91 recognition site.

XX
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
 |||||
 Db 1 RNNVLIQTDDQATTR 15

RESULT 2
 AAM50103
 ID AAM50103 standard; protein; 424 AA.
 XX
 AC AAM50103;
 XX
 XX 02-SEP-2002 (first entry)
 XX
 XX Equine IgE heavy chain constant region C-epsilon allotype A.
 DE
 DE Cea; equine; horse; heavy chain; constant region; allotype a; IgE;
 KW C-epsilon a; immunoglobulin E; antiallergic; allergy.
 XX
 XX Equus caballus.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT Domain 1..97
 FT /note= "CH1 domain"
 FT Domain 98..205
 FT /note= "CH2 domain"
 FT Domain 206..312
 FT /note= "CH3 domain"
 FT Domain 313..424
 FT /note= "CH4 domain"
 FT
 FN WO200250280-A2.
 XX
 XX 27-JUN-2002.
 XX
 XX 20-DEC-2001; 2001WO-DE004810.
 XX
 XX 21-DEC-2000; 2000DE-01064415.
 XX
 XX (TIER-) TIERAERTLICHE HOCHSCHULE HANNOVER.
 XX
 XX Leibold W, Wagner B, Radbruch A;
 XX
 XX WPI; 2002-508803/54.
 DR N-PSDB; ABL61246.
 XX
 XX DNA sequence encoding part of an equine immunoglobulin G, useful for
 XX preparing isotype-specific antibodies for diagnosis and treatment of
 XX allergy in horses.
 XX
 XX Claim 1; Page 31-32; 37pp; German.
 XX
 XX This invention describes a novel DNA (I) encoding the constant region
 XX (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The
 XX products of the invention are capable of neutralising IgE activity and
 XX have antiallergic activity. The polynucleotides of the invention are used
 XX to produce recombinant IgE (II), and this is used to raise specific
 XX monoclonal antibodies (MAB). Both (II) and MAB are useful for diagnosis,
 XX particularly of allergy in horses, and MAB can also be used for treatment
 XX of allergies. (I) make possible production of isotype-specific
 XX antibodies, important for precise evaluation of the immune response. This
 XX sequence represents a fragment of the equine IgE heavy chain constant
 XX region C-epsilon allotype a (Ceb), used in the method of the invention
 XX for IgE-isotype recombinant immunoglobulin production

CC sequence represents a fragment of the equine IgE heavy chain constant
 CC region C-epsilon allotype a (Cea), used in the method of the invention
 CC for IgE-isotype recombinant immunoglobulin production

XX
 XX
 SQ Sequence 424 AA;

Query Match 100.0%; Score 74; DB 5; Length 424;
 Best Local Similarity 100.0%; Pred. No. 8.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
 |||||
 Db 356 RNNVLIQTDDQATTR 370

RESULT 3
 AAM50104
 ID AAM50104 standard; protein; 424 AA.
 XX
 AC AAM50104;
 XX
 XX 02-SEP-2002 (first entry)
 XX
 XX Equine IgE heavy chain constant region C-epsilon allotype b.
 XX
 XX Ceb; equine; horse; heavy chain; constant region; allotype b; IgE;
 KW C-epsilon b; immunoglobulin E; antiallergic; allergy.
 XX
 XX Equus caballus.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT Domain 1..97
 FT /note= "CH1 domain"
 FT Domain 98..205
 FT /note= "CH2 domain"
 FT Domain 206..312
 FT /note= "CH3 domain"
 FT Domain 313..424
 FT /note= "CH4 domain"
 FT
 FN WO200250280-A2.
 XX
 XX 27-JUN-2002.
 XX
 XX 20-DEC-2001; 2001WO-DE004810.
 XX
 XX 21-DEC-2000; 2000DE-01064415.
 XX
 XX (TIER-) TIERAERTLICHE HOCHSCHULE HANNOVER.
 XX
 XX Leibold W, Wagner B, Radbruch A;
 XX
 XX WPI; 2002-508803/54.
 DR N-PSDB; ABL61247.
 XX
 XX DNA sequence encoding part of an equine immunoglobulin G, useful for
 XX preparing isotype-specific antibodies for diagnosis and treatment of
 XX allergy in horses.
 XX
 XX Claim 1; Page 34-36; 37pp; German.
 XX
 XX This invention describes a novel DNA (I) encoding the constant region
 XX (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The
 XX products of the invention are capable of neutralising IgE activity and
 XX have antiallergic activity. The polynucleotides of the invention are used
 XX to produce recombinant IgE (II), and this is used to raise specific
 XX monoclonal antibodies (MAB). Both (II) and MAB are useful for diagnosis,
 XX particularly of allergy in horses, and MAB can also be used for treatment
 XX of allergies. (I) make possible production of isotype-specific
 XX antibodies, important for precise evaluation of the immune response. This
 XX sequence represents a fragment of the equine IgE heavy chain constant
 XX region C-epsilon allotype b (Ceb), used in the method of the invention
 XX for IgE-isotype recombinant immunoglobulin production

XX SQ Sequence 424 AA;
Query Match 100.0%; Score 74; DB 5; Length 424;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RNNVLIQTDOQATTR 15
Db 356 RNNVLIQTDOQATTR 370

RESULT 4
AED15438
ID AED15438 standard; protein; 566 AA.
XX AC AED15438;
XX DT 01-DEC-2005 (first entry)
XX DE Equine Protozoal Myeloencephalitis marker polypeptide, SEQ ID No:21.
XX KW equine protozoal myeloencephalitis; genetic marker; diagnosis;
XX KW sarcocystis neuropa infection; protozoacide.
XX OS Equidae.
XX PN WO2005090593-A1.
XX PD 29-SEP-2005.
XX PF 21-MAR-2005; 2005WO-AU000401.
XX PR 19-MAR-2004; 2004AU-00901448.
XX PR 29-MAR-2004; 2004US-0556869P.
XX PR 23-JUN-2004; 2004US-0581840P.
XX PA (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX PI Brandon RB, Thomas MR;
XX WPI; 2005-659146/67.
XX DR N-PSDB; AED15437.
XX PT New isolated Equine Protozoal Myeloencephalitis (EPM) marker
XX PT polynucleotides and polypeptides, useful in diagnosing, monitoring and
XX PT treating EPM in affected animals, e.g. horse.
XX PS Claim 1; SEQ ID NO 21; 356pp; English.

XX CC The invention relates to isolated Equine Protozoal Myeloencephalitis
XX CC (EPM) marker polynucleotide sequences selected from any of the fully
XX CC defined sequences (SEQ ID NOS 1, 3, 5, 7, 8, 10, 12, 14, 16, 17, 18, 20,
XX CC 22, 24, 26, 27, 28, 30, 32, 34-50, 52, 54, 55, 56, 57, or 422) in the
XX CC specification. The EPM polynucleotide sequences encode EPM polypeptides
XX CC (SEQ ID NOS 2, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 35, 53,
XX CC or 58). Also described are: (1) a method of diagnosing the presence of
XX CC EPM or Sarcocystis neuropa infection in a test subject; (2) a method of
XX CC treating, preventing, or inhibiting the development of EPM in a subject;
XX CC (3) a nucleic acid construct comprising an EPM marker polynucleotide in
XX CC operable connection with a regulatory element that is operable in a host
XX CC cell; (4) an isolated host cell containing the nucleic acid construct;
XX CC (5) a probe (SEQ ID NO. 59-421) comprising a nucleotide sequence that
XX CC hybridizes under low stringency conditions to the polynucleotide; and (6)
XX CC a solid or semi-solid support comprising at least one probe immobilized
XX CC on it. The EPM marker polynucleotides, probes, EPM marker polypeptides,
XX CC or antigen-binding molecules that are immuno-interactive with the EPM
XX CC marker polypeptide, are useful for diagnosing the presence of EPM in a
XX CC subject. The EPM marker polynucleotides and polypeptides are also useful
XX CC for the diagnosis, monitoring, and treatment of EPM in affected animals.
XX CC This sequence represents an EPM marker polypeptide.

XX SQ Sequence 566 AA;
Query Match 100.0%; Score 74; DB 9; Length 566;
Best Local Similarity 100.0%; Pred. NO. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RNNVLIQTDOQATTR 15
Db 499 RNNVLIQTDOQATTR 513

RESULT 5
AEE88000
ID AEE88000 standard; protein; 566 AA.
XX AC AEE88000;
XX DT 23-FEB-2006 (first entry)
XX DE Human protein sequence #49.
XX KW Diagnosis; immunity; stress; psychiatric disorder; tranquilizer.
XX OS Homo sapiens.
XX PN WO2005118810-A1.
XX PD 15-DEC-2005.
XX PF 03-JUN-2005; 2005WO-AU000794.
XX PR 03-JUN-2004; 2004US-0576285P.
XX PR 04-JUN-2004; 2004AU-00903003.
XX PA (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX PI Brandon RB, Thomas MR;
XX WPI; 2006-039470/04.
XX DR N-PSDB; AEE87999.
XX PT Determining presence or degree of a physiological response to stress or a
XX PT related condition in a test subject, comprises detecting in the test
XX PT subject aberrant expression of at least one stress marker gene.
XX PS Claim 1; SEQ ID NO 136; 445pp; English.

XX CC The invention relates to a method of determining the presence or degree
XX CC of a physiological response to stress or a related condition in a test
XX CC subject comprising detecting in the test subject aberrant expression of
XX CC at least one stress marker gene given in the specification. The invention
XX CC also relates to a method of treating, preventing or inhibiting the
XX CC development of stress in a subject, an isolated stress marker
XX CC polynucleotide, a nucleic acid construct comprising a stress marker
XX CC polynucleotide in operable connection with a regulatory element that is
XX CC operable in a host cell, an isolated host cell containing the construct,
XX CC a probe comprising a nucleotide sequence that hybridizes under at least
XX CC low stringency conditions to the marker polynucleotide and a solid or
XX CC semi-solid support comprising at least one probe immobilized on it. The
XX CC stress marker polynucleotides, probes, stress marker polypeptides or
XX CC antigen-binding molecules that are immuno-interactive with the stress
XX CC marker polypeptide are useful for the manufacture of a kit for diagnosing
XX CC the presence of a physiological response to stress in a subject. The
XX CC methods are useful for determining the presence or degree of a
XX CC physiological response to stress or a related condition in a test
XX CC subject, and for treating, preventing or inhibiting the development of
XX CC stress in a subject. The physiological response to stress is selected
XX CC from physical stress, mood disorders, anxiety disorders, inflammation,
XX CC pain, chronic fatigue syndrome, stress-induced headache, cancer, human
XX CC immunodeficiency virus (HIV) infections, neurodegenerative diseases,
XX CC gastrointestinal diseases, eating disorders, supranuclear palsy,
XX CC ankyrotrophic lateral sclerosis, a decrease in immune function or
XX CC immunosuppression, hemorrhagic stress, stress-induced psychotic episodes,
XX CC euthyroid sick syndrome, syndrome of inappropriate antidiuretic hormone

CC (ADH), overeating or obesity, infertility, head traumas, spinal cord
 CC trauma, ischemic neuronal damage, excitotoxic neuronal damage, epilepsy,
 CC cardiovascular diseases, stroke, immune dysfunctions, muscular spasms,
 CC urinary incontinence, senile dementia, Alzheimer's disease, multi-infarct
 CC dementia, amyotrophic lateral sclerosis, chemical dependencies and
 CC addictions, drug and alcohol withdrawal symptoms, osteoporosis,
 CC psychosocial dwarfism, hypoglycemia, hair loss, abnormal circadian rhythm
 CC or disorders related to abnormal circadian rhythm. This sequence
 CC represents a human protein used in the method of the invention.
 XX
 SQ Sequence 566 AA;

Query Match 100.0%; Score 74; DB 10; Length 566;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
 Db 499 RNNVLIQTDDQATTR 513

RESULT 6
 ABP96585
 ID ABP96585 standard; protein; 569 AA.

AC ABP96585;

XX
 XX
 DT 28-MAY-2003 (first entry)

DE Horse IgE heavy chain amino acid sequence SEQ ID NO:30.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW anti-allergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
 KW dermatologic; antiinflammatory; IgE-mediated condition; food allergy;
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KW urticaria hives.

XX Equus caballus.

XX WO2003015716-A2.

XX
 XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IgE, by identifying peptide eliciting CTL response to IgE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.

PS Example 7; Page 157-160; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IgE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IgE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to

CC elicit in a mammal a CTL response to naturally processed and presented
 CC IgE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IgE, and in
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IgE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 XX
 SQ Sequence 569 AA;

Query Match 100.0%; Score 74; DB 6; Length 569;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
 Db 501 RNNVLIQTDDQATTR 515

RESULT 7
 ADC64568

ID ADC64568 standard; peptide; 15 AA.

XX
 AC ADC64568;

XX 18-DEC-2003 (first entry)

XX Horse immunoglobulin E, IgE, heavy chain immunogenic peptide P4.

DE
 XX Horse; immunoglobulin E; IgE; heavy chain; immunogen; allergy.

KW Equus caballus.

XX US2003087314-A1.

XX 08-MAY-2003.

XX 08-NOV-2001; 2001US-00052788.

XX 08-NOV-2001; 2001US-00052788.

XX (REGC) UNIV CALIFORNIA.

XX Gershwin LJ, Pettigrew HD, Kalina WV;

XX WPI; 2003-765437/72.

XX Immunogenic composition comprising an isolated equine immunoglobulin E
 PT polypeptide that induces production of antibodies which specifically bind
 PT to equine immunoglobulin E.

XX Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an
 CC isolated polypeptide having an amino acid sequence that is at least 80%
 CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
 CC equine immunoglobulin E (the composition induces production of an
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six
 CC polypeptides are not explicitly identified in the specification. Also
 CC included are a composition comprising an antibody that specifically binds
 CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
 CC specifically binds to equine IgE made by the process of immunising an
 CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an
 CC antibody that specifically binds to equine IgE (involving immunising an
 CC animal with a composition further comprising an isolated polypeptide (the
 CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-
 CC (S6)), and collecting antiserum from the animal) and a kit for detection

CC of equine IgE in a biological sample comprising the antibody and means
 CC for detecting specific binding of the antibody to equine IgE. The
 CC antibody is useful for detecting equine IgE protein in a biological
 CC sample (serum) which involves contacting the sample with the antibody,
 CC thus forming an antigen/antibody complex, and detecting the presence or
 CC absence of the antigen/antibody complex. The antibody and antigen are
 CC immobilised on a solid surface. The antibody is labelled such that the
 CC complex can be detected. The complex is detected using a second labelled
 CC antibody. The peptides are useful for generating antibodies specific for
 CC IgE which can serve as a diagnostic test for allergy. The present
 CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic
 CC peptide from the early portion of the C4 region.
 XX
 SQ Sequence 15 AA;

Query Match 66.2%; Score 49; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.074;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IQTDDQATTR 15
 Db 1 IQTDDQATTR 10
 |||||

RESULT 8

AEB39722
 ID AEB39722 standard; protein; 417 AA.

XX AC AEB39722;

XX DT 08-SEP-2005 (first entry)

XX DE L. pneumophila protein SEQ ID NO 4054.

XX KW detection; infection; Antibacterial; Vaccine.

XX OS Legionella pneumophila.

XX PN WO2005049642-A2.

XX PD 02-JUN-2005.

XX PF 23-SEP-2004; 2004WO-IB003578.

XX PR 21-NOV-2003; 2003FR-00013687.

XX PA (INSP) INST PASTEUR.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 XX PI Rueniock C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 XX PI Jarraud S;

XX WPI; 2005-388305/40.

XX PT New genome of Legionella pneumophila Paris strain and derived
 XX PT polypeptides, useful for detection or identification of the strain and
 XX PT for treatment and prevention of infections.

XX PS Claim 3; SEQ ID NO 4054; 660pp; English.

XX CC The invention relates to an isolated or purified nucleotide sequences (I)
 XX CC from Legionella pneumophila Paris strain. (I), and their related
 XX CC sequences or fragments, are useful as primers and probes for detection
 XX CC and amplification, including differentiation between the Paris and
 XX CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
 XX CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 XX CC specific antibodies (Ab), also used for detection/identification of
 XX CC Legionella, and some (I), specifically those involved in synthesis of
 XX CC surface proteins, are targets for identification of inhibitors. (II), or
 XX CC vectors that contain (I), are useful as vaccines and immunogenic

CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.
 XX
 SQ Sequence 417 AA;

Query Match 58.1%; Score 43; DB 9; Length 417;
 Best Local Similarity 69.2%; Pred. No. 38;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIQDQQAATT 14
 Db 63 NNVLIPLEQQPTT 75
 ||||| :|||

RESULT 9

AEB36305
 ID AEB36305 standard; protein; 452 AA.

XX AC AEB36305;

XX DT 08-SEP-2005 (first entry)

XX DE L. pneumophila protein SEQ ID NO 637.

XX KW detection; infection; Antibacterial; Vaccine.

XX OS Legionella pneumophila.

XX PN WO2005049642-A2.

XX PD 02-JUN-2005.

XX PF 23-SEP-2004; 2004WO-IB003578.

XX PR 21-NOV-2003; 2003FR-00013687.

XX PA (INSP) INST PASTEUR.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 XX PI Rueniock C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 XX PI Jarraud S;

XX WPI; 2005-388305/40.

XX PT New genome of Legionella pneumophila Paris strain and derived
 XX PT polypeptides, useful for detection or identification of the strain and
 XX PT for treatment and prevention of infections.

XX PS Claim 3; SEQ ID NO 637; 660pp; English.

XX CC The invention relates to an isolated or purified nucleotide sequences (I)
 XX CC from Legionella pneumophila Paris strain. (I), and their related
 XX CC sequences or fragments, are useful as primers and probes for detection
 XX CC and amplification, including differentiation between the Paris and
 XX CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
 XX CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 XX CC specific antibodies (Ab), also used for detection/identification of
 XX CC Legionella, and some (I), specifically those involved in synthesis of
 XX CC surface proteins, are targets for identification of inhibitors. (II), or
 XX CC vectors that contain (I), are useful as vaccines and immunogenic
 XX CC compositions, for treatment and prevention of infections by L.
 XX CC pneumophila. The present sequence represents the amino acid sequence of a
 XX CC L. pneumophila protein.

XX SQ Sequence 452 AA;

Query Match 58.1%; Score 43; DB 9; Length 452;
 Best Local Similarity 69.2%; Pred. No. 41;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY      2 NNVLITDQQAATT 14
Db      98 NNVLIFLEQQPTT 110

RESULT 10
ABG32001
ID  ABG32001 standard; protein; 580 AA.
XX
AC  ABG32001;
XX
XX  06-AUG-2003 (revised)
DT  15-NOV-2002 (first entry)
XX
XX  Q. intestinalis arginine deiminase gene, QIAADIINT.
DE
XX  Arginine deiminase; cytostatic; ADI; polyethylene glycol; PEG; arginine;
KW  citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;
KW  auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.
XX
XX  Giardia intestinalis.
OS
XX  WO200244360-A2.
PN
XX  06-JUN-2002.
PD
XX  19-SEP-2001; 2001WO-US029184.
PF
XX  28-NOV-2000; 2000US-00723546.
PR
XX  (PHOE-) PHOENIX PHARMACOLOGICS INC.
PA
XX  Clark MA;
PI
XX  WPI; 2002-619003/66.
DR
XX  Compound for treating tumor such as melanoma, hepatoma or sarcoma in a
PT  patient, comprises arginine deiminase covalently bonded by a linking
PT  group such as succinimide to polyethylene glycol.
XX
PS  Disclosure; Fig 12; 59pp; English.
XX
XX  The invention discloses a compound comprising arginine deiminase (ADI)
CC  covalently bonded by a linking group to polyethylene glycol (PEG) having
CC  a total weight average molecular weight of about 1000-50000. Also
CC  disclosed is a method for enhancing the circulating half life or the
CC  tumoricidal activity of arginine deiminase by modifying the arginine
CC  deiminase by covalently bonding the arginine deiminase by a linking group
CC  to PEG. Normal cells can synthesise arginine from citrulline in a 2 step
CC  process catalysed by argininosuccinate synthase and argininosuccinate
CC  lyase. In contrast, many cancerous cells do not express argininosuccinate
CC  synthase and are, therefore, auxotrophic for arginine. Arginine deiminase
CC  catalyses the conversion of arginine to citrulline and can be used to
CC  eliminate arginine from the cancerous cells. The compound is useful for
CC  treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or
CC  for treating and inhibiting metastases in a patient. When compared to
CC  native arginine deiminase the compound retains most of its enzymatic
CC  activity, is far less antigenic, has a greatly extended circulating half-
CC  life, and is much more efficacious in the treatment of tumours. The
CC  sequence presented is the Giardia intestinalis arginine deiminase gene,
CC  QIAADIINT. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ  Sequence 580 AA;

Query Match      58.1%; Score 43; DB 5; Length 580;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 NNVLITDQQAATT 15
Db      168 NNWVFRDQQTTR 181

RESULT 11
ADP79623
ID  ADP79623 standard; protein; 580 AA.
XX
XX  ADP79623;
AC
XX  04-NOV-2004 (first entry)
DT
XX  Giardia intestinalis arginine deiminase.
DE
XX  Arginine deiminase; cytostatic; virucide; viral replication;
KW  nitric oxide synthesis; tumour; liver function; enzyme.
XX
XX  Giardia intestinalis.
OS
XX  WO2004046309-A2.
PN
XX  03-JUN-2004.
PD
XX  29-SEP-2003; 2003WO-US030770.
PF
XX  18-NOV-2002; 2002US-0427497P.
PR
XX  (PHOE-) PHOENIX PHARMACOLOGICS INC.
PA
XX  Clark MA;
PI
XX  WPI; 2004-431965/40.
DR
XX  Inhibiting replication of viruses in individual, involves administering
PT  composition comprising arginine deiminase bonded to polyethylene glycol,
PT  to individual.
XX
XX  Claim 18; SEQ ID NO 17; 89pp; English.
XX
XX  The invention relates to inhibiting the replication of one or more
CC  viruses in an individual and involves administering to the individual a
CC  composition comprising an arginine deiminase bonded to polyethylene
CC  glycol. The method is useful for inhibiting replication of one or more
CC  viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,
CC  where the arginine deiminase is derived from Mycoplasma e.g. M. arginini,
CC  M. hominis, M. arthritidis and its combination. It is useful for treating
CC  an individual who is suspected of having been exposed to one or more
CC  viruses, for modulating nitric oxide levels in an individual, or for
CC  selectively inhibiting viral replication in an individual. The method is
CC  also useful for treating a tumour and inhibiting replication of one ore
CC  more viruses in an individual. The tumour is melanoma, sarcoma, or
CC  hepatoma. The tumour is hepatocellular carcinoma. The method is also
CC  useful for improving liver function in an individual. The present
CC  sequence represents a Giardia intestinalis arginine deiminase.
XX
SQ  Sequence 580 AA;

Query Match      58.1%; Score 43; DB 8; Length 580;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 NNVLITDQQAATT 15
Db      168 NNWVFRDQQTTR 181

RESULT 12
ADRI0601
ID  ADRI0601 standard; peptide; 15 AA.
XX
XX  ADRI0601;
AC
XX  21-OCT-2004 (first entry)
DT
XX  Dog IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
XX
```

KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
 XX
 OS Canis familiaris.
 XX
 PN WO2004065936-A2.
 XX
 PD 05-AUG-2004.
 XX
 XX 15-JAN-2004; 2004WO-US003566.
 PF
 XX 16-JAN-2003; 2003US-0440472P.
 PR
 XX (UUNC-) UNIV NORTH CAROLINA STATE.
 PA
 XX Hammerberg B;
 XX
 XX WPI; 2004-593545/57.
 DR
 XX Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.
 XX
 XX Example 6; Page 9; 14pp; English.
 PS
 XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE.
 XX
 SQ Sequence 15 AA;
 Query Match 55.4%; Score 41; DB 8; Length 15;
 Best Local Similarity 64.3%; Pred. No. 2.1;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RNNVLIQTDDQATT 14
 ||: ||||| ||
 DB 1 RNDSPITQDQYTTT 14
 RESULT 13
 AAY79995
 ID AAY79995 standard; protein; 312 AA.
 XX
 AC AAY79995;
 XX
 DT 15-MAY-2000 (first entry)
 XX
 DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
 XX
 XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX
 OS Canis sp.
 XX
 XX WO9967293-A1.
 PN
 XX 29-DEC-1999.
 PD
 XX

PF 21-JUN-1999; 99WO-US013959.
 XX
 XX 20-JUN-1998; 98US-00100287.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY, Walfield AM;
 XX
 DR WPI; 2000-160578/14.
 XX
 XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy.
 PT
 XX Example 1; Page 66-68; 155pp; English.
 PS
 XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IgE, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 312 AA;
 Query Match 55.4%; Score 41; DB 3; Length 312;
 Best Local Similarity 64.3%; Pred. No. 63;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RNNVLIQTDDQATT 14
 ||: ||||| ||
 DB 255 RNDSPITQDQYTTT 268
 RESULT 14
 ADN24060
 ID ADN24060 standard; protein; 312 AA.
 XX
 AC ADN24060;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #6713.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 PN
 XX 18-DEC-2003.
 PD
 XX 20-FEB-2003; 2003US-00369493.
 XX
 XX 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 8.93939 Seconds
(without alignments)
161.448 Million cell updates/sec

Title: US-10-758-165a-3

Perfect score: 74

Sequence: 1 RNNVLITDQQAATT 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1.*
- 2: Pir2.*
- 3: Pir3.*
- 4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	60.8	917	2 F95884	probable sensory h
2	43.5	58.8	285	2 H84219	hypothetical prote
3	43	58.1	580	2 T45064	arginine deiminase
4	41	55.4	312	2 T32446	hypothetical prote
5	41	55.4	312	2 A89460	protein H42K12.1 [
6	41	55.4	2145	2 S61041	glutamate synthase
7	39	52.7	263	2 E85042	hypothetical prote
8	39	52.7	716	2 H84421	probable receptor-
9	38	51.4	138	2 G97191	probable membrane
10	38	51.4	829	2 A12531	hypothetical prote
11	38	51.4	1827	1 A23945	sucrose alpha-gluc
12	37	50.0	128	1 H64842	probable translati
13	37	50.0	128	2 F90785	hypothetical prote
14	37	50.0	128	2 F85645	hypothetical prote
15	36.5	49.3	1017	2 S67804	LRG1 protein - yea
16	36	48.6	140	2 S72252	hemoglobin, extrac
17	36	48.6	205	2 B88095	protein F39E9.5 [1
18	36	48.6	407	2 A21150	serine proteinase
19	36	48.6	412	2 T24441	hypothetical prote
20	36	48.6	433	2 C70163	GTP-binding protei
21	36	48.6	441	2 G98136	histidine protein
22	36	48.6	441	2 B95261	probable sensor hi
23	36	48.6	468	2 A53889	protein-tyrosine-p
24	36	48.6	468	2 T43622	targeted effector
25	36	48.6	468	2 S01054	virulence protein
26	36	48.6	487	1 S07062	glutamate receptor
27	36	48.6	487	2 T51201	kinase-binding pr
28	36	48.6	962	2 C81060	translation initia
29	36	48.6	967	2 C70831	probable mmpL4 pro

30	36	48.6	1157	2 AD1728	ATP-dependent deox
31	36	48.6	1418	2 T15232	hypothetical prote
32	36	48.6	1449	2 T20181	hypothetical prote
33	36	48.6	1464	2 JC5144	murinoglobulin pre
34	36	48.6	1584	2 T20180	hypothetical prote
35	36	48.6	1586	2 T20179	hypothetical prote
36	36	48.6	2021	2 AD2267	serins/threonine k
37	35	47.3	185	2 T14523	hypothetical prote
38	35	47.3	225	2 AC0587	KOP operon transcr
39	35	47.3	225	2 B90719	transcription regu
40	35	47.3	225	2 C85569	hypothetical prote
41	35	47.3	225	2 E64804	transcription regu
42	35	47.3	252	2 T20321	hypothetical prote
43	35	47.3	276	2 B84597	probable disease r
44	35	47.3	345	2 S73498	MG456 homolog K05
45	35	47.3	386	2 T09019	phosphoprotein pho

ALIGNMENTS

RESULT 1

F95884

probable sensory histidine kinase protein [imported] - Sinorhizobium meliloti (strain 10

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: F95884

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: F95884

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-917 <KUR>

A;Cross-references: UNIPROT:Q92WJ7; UNIPARC:UPI00000CB4C5; GB:AL591985; PIDN:CAC48742.1;

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.K.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.;

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: Smb20356

A;Genome: plasmid

Query Match 60.8%; Score 45; DB 2; Length 917;

Best Local Similarity 57.1%; Pred. No. 3.6;

Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNNVLITDQQAATT 14

Db 188 RNEVVVQTEKTAAT 201

RESULT 2

H84219

hypothetical protein Vng0617h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: H84219

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: H84219

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <STO>
A;Cross-references: UNIPROT:Q9HRN4; UNIPARC:UPI00000636A7; GB:AE004437; NID:gi10580210; P
C;Genetics:
A;Gene: VNG0617H

Query Match 58.8%; Score 43.5; DB 2; Length 285;
Best Local Similarity 58.8%; Pred. No. 1.8;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 2 NNVLQTDQ--ATTR 15
|||||:|:|:|
Db 212 NNVLQTDSEVELTTR 228
|||||:|:|:|

RESULT 3
T45064
arginine deiminase (EC 3.5.3.6) [validated] - Giardia intestinalis
C;Species: Giardia intestinalis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45064
R;Knudler, L.A.; Skyeve, E.O.; Stewart, T.S.; Schofield, P.J.; Edwards, M.R.
J. Biol. Chem. 273, 4470-4477, 1998
A;Title: Cloning and expression of a prokaryotic enzyme, arginine deiminase, from a prim
A;Reference number: Z22902; MUID:98136144; PMID:9468500
A;Accession: T45064
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-580 <KNO>
A;Cross-references: UNIPROT:Q27657; UNIPARC:UPI000004CCBB; EMBL:U49236; PIDN:AAC06116.1
A;Experimental source: strain Fortland 1
C;Function:
A;Description: EC 3.5.3.6 [validated, MUID:98136144]
C;Superfamily: Giardia intestinalis arginine deiminase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 580;
Best Local Similarity 57.1%; Pred. No. 5.2;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLQTDQQAATTR 15
||:|:|:|:|
Db 168 NNWFMRDQAATTR 181
||:|:|:|:|

RESULT 4
T32446
hypothetical protein H42K12.1 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Oct-2004
C;Accession: T32446
R;Maggi, L.; Harper, M.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid H42K12.
A;Reference number: Z21169
A;Accession: T32446
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-312 <MAG>
A;Cross-references: UNIPARC:UPI000017A469; EMBL:AF026207; PIDN:AAB71265.1; GSPDB:GN00028
A;Experimental source: strain Bristol N2; clone H42K12
C;Genetics:
A;Gene: CESP:H42K12.1
A;Map position: X
A;Introns: 4/2; 40/3; 106/1; 167/1; 196/2; 251/3

Query Match 55.4%; Score 41; DB 2; Length 312;
Best Local Similarity 57.1%; Pred. No. 6.1;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLQTDQQAATTR 15
|||||:|:|:|

Db 159 DNVLQKDEENTAR 172

RESULT 5

A89460

protein H42K12.1 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 31-Dec-2004

C;Accession: A89460

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: A89460

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-312 <STO>

A;Cross-references: UNIPARC:UPI000017A469; GB:chr_X; PIDN:AAB71265.1; PID:92435556; GSPDB:

A;Note: Similar to protein kinase

C;Genetics:

A;Gene: H42K12.1

A;Map position: X

Query Match

55.4%; Score 41; DB 2; Length 312;

Best Local Similarity 57.1%; Pred. No. 6.1;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLQTDQQAATTR 15

:|||||:|:|:|

Db 159 DNVLQKDEENTAR 172

RESULT 6

S61041

glutamate synthase (NADH2) (EC 1.4.1.14) gltI precursor [similarity] - yeast (Saccharomy

N;Alternate names: protein D1448; protein YDL171c

C;Species: Saccharomyces cerevisiae

C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 12-Jul-2004

C;Accession: S61041; S67723

R;Pohl, T.M.

submitted to the EMBL Data Library, November 1995

A;Reference number: S61010

A;Accession: S61041

A;Molecule type: DNA

A;Residues: 1-2145 <POH>

A;Cross-references: UNIPARC:UPI00001682D6; EMBL:Z67750; NID:gi1061256; PIDN:CAA91574.1; P

R;Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67708

A;Accession: S67723

A;Molecule type: DNA

A;Residues: 1-2145 <POW>

A;Cross-references: UNIPARC:UPI00001682D6; EMBL:Z74219; NID:gi1431273; PIDN:CAA98745.1; P

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGB:GLT1

A;Cross-references: SGD:S0002330; MIPS:YDL171c

A;Map position: 4L

C;Superfamily: glutamate synthase (NADH/NADPH), eukaryotic type

C;Keywords: 3Fe-4S; metalloprotein; oxidoreductase; transmembrane protein

F;1-53/Domain: propeptide #status predicted <PRO>

F;54-2145/Product: glutamate synthase #status predicted <MAT>

F;1077-1093/Domain: transmembrane #status predicted <TM1>

F;1172-1188/Domain: transmembrane #status predicted <TM2>

F;54/Active site: Cys #status predicted

F;1185,1191,1196/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match

55.4%; Score 41; DB 2; Length 2145;

Best Local Similarity 57.1%; Pred. No. 55;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLQTDQQAATTR 15

:|||||:|:|:|

Qy 1 RNNVLIQTDOQATT 14
| : : : : : |
Db 1145 RNNVVQTGQLRT 1158

RESULT 7
E85042
hypothetical protein AT4g03350 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E85042
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: E85042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <STO>
A;Cross-references: UNIPROT:Q9ZQZ6; UNIPARC:UPI00000A63C9; GB:NC_001268; NID:g7270205; E
C;Genetics:
A;Gene: AT4g03350
A;Map position: 4

Query Match 52.7%; Score 39; DB 2; Length 263;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQATT 14
| : : : : : |
Db 145 RTNQVVQTTEQAST 158

RESULT 8
H84421
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C;Accession: H84421
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84421
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-716 <STO>
A;Cross-references: UNIPROT:Q9ZU46; UNIPARC:UPI00000A1C90; GB:AE002093; NID:g4262228; PT
C;Genetics:
A;Gene: At2g01210
A;Map position: 2
C;Superfamily: Receptor-like protein kinase

Query Match 52.7%; Score 39; DB 2; Length 716;
Best Local Similarity 53.3%; Pred. No. 38;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQATT 15
: : : : : |
Db 568 QSNRIIQTDOQPQR 582

RESULT 9
G97191
probable membrane protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97191
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4836, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97191
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-138 <KUR>
A;Cross-references: UNIPROT:Q97GK0; UNIPARC:UPI00000CA4D0; GB:AE001437; PIDN:AAK80322.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2366

Query Match 51.4%; Score 38; DB 2; Length 138;
Best Local Similarity 53.8%; Pred. No. 9;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQOQATT 14
| : : : : : |
Db 42 NNILAQSGQAST 54

RESULT 10
AI2531
hypothetical protein alr7540 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AI2531
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2531
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-829 <KUR>
A;Cross-references: UNIPROT:Q8ZSH0; UNIPARC:UPI00000CCD69; GB:AP003602; PIDN:BA877183.1;
C;Genetics:
A;Experimental source: strain PCC 7120

Query Match 51.4%; Score 38; DB 2; Length 829;
Best Local Similarity 70.0%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NNVLITDQOQ 11
| : : : : : |
Db 591 NNVLIQADKE 600

RESULT 11
A23945
sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) - rabbit
N;Alternate names: small intestinal sucrase/isomaltase (SI)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 24-May-1996
C;Accession: A23945; B25987; A29163
R;Hunziker, W.; Spiess, M.; Semenza, G.; Lodish, H.F.
Cell 46, 227-234, 1986
A;Title: The sucrase-isomaltase complex: primary structure, membrane-orientation, and ev
A;Reference number: A23945; MUID:86245068; PMID:3755079
A;Accession: A23945
A;Molecule type: mRNA
A;Residues: 1-1827 <HUN>
A;Cross-references: UNIPARC:UPI00001729E8
R;Stoetrom, H.; Noren, O.; Christensen, L.A.; Wacker, H.; Spiess, M.; Bigler-Meier, B.
FEBS Lett. 148, 321-325, 1982
A;Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-sucrase-isoma
A;Reference number: A25987; MUID:83105704; PMID:7152027
A;Accession: B25987
A;Molecule type: protein
A;Residues: 2-32, 'XXX', 36-38; 1008, 'N', 1010-1014, 'E' <SU2>

C;Cross-references: UNIPARC:UPI00001729E9; UNIPARC:UPI00001729EA
R;Frank, G.; Brunner, J.; Jauser, H.; Wacker, H.; Semenza, G.; Zuber, H.
FEBS Lett. 96, 183-188, 1978
A;Title: The hydrophobic anchor of small-intestinal sucrase-isomaltase. N-terminal sequence
A;Reference number: A29163; MUID:79086207; PMID:729784
A;Accession: A29163
A;Molecule type: protein
A;Residues: 2, 'VNA', 6-32, 'XXX', 36-38 <FRA>
A;Cross-references: UNIPARC:UPI00001729EB
C;Comment: Carbohydrate analysis of the mature enzyme complex indicates both N- and O-linked
C;Complex: the two product chains remain associated after cleavage
C;Function: <ISM>
A;Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic
A;Pathway: carbohydrate digestion
C;Function: <SUC>
A;Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glucose
A;Pathway: carbohydrate digestion
C;Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology
C;Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m
F;2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental <ISO>
F;13-32/Domain: membrane associated #status predicted <TMW>
F;43-65/Region: serine/threonine-rich
F;63-109/Domain: trefoil homology <TRF1>
F;189-840/Domain: sucrase/isomaltase homology <SIM>
F;931-977/Domain: trefoil homology <TRF2>
F;1008-1827/Product: sucrose alpha-glucosidase (sucrase chain) #status experimental <SUC>
F;1062-1734/Domain: sucrase/isomaltase homology <SM2>
F;12/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;99,455,859,896,904,1235,1303,1325,1340,1354,1368,1403,1535,1572,1748,1763,1799/Binding
F;1007-1008/Cleavage site: Arg-Ile (trypsin) #status predicted

Query Match 51.4%; Score 38; DB 1; Length 1827;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NNVLITDQQAQTR 15
||||| : |||
Db 144 NNVLTTESQANR 157

RESULT 12
H64842
Probable translation initiation regulator b1010 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: H64842
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64842
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-128 <BLAT>
A;Cross-references: UNIPROT:P75896; UNIPARC:UPI000013ASE1; GB:AE000202; GB:U00096; NID:9
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: translation initiation inhibitor, TdcF type

Query Match 50.0%; Score 37; DB 1; Length 128;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NNVLITDQQAQTR 15
||||| : |||
Db 40 NNVLFDADPKAQTR 53

RESULT 13
H90785
Hypothetical protein ECs1256 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004

C;Accession: H90785
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A96629; MUID:21156231; PMID:11258796
A;Accession: H90785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <HAY>
A;Cross-references: UNIPROT:Q8XAU5; UNIPARC:UPI00000D067E; GB:BA000007; PIDN:BAB34679.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1256
C;Superfamily: translation initiation inhibitor, TdcF type

Query Match 50.0%; Score 37; DB 2; Length 128;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NNVLITDQQAQTR 15
||||| : |||
Db 40 NNVLFDADPKAQTR 53

RESULT 14
F85645
Hypothetical protein Z1509 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C;Accession: F85645
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F85645
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <STO>
A;Cross-references: UNIPROT:Q8XAU5; UNIPARC:UPI00000D067E; GB:AE005174; NID:gl2514367; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1509
C;Superfamily: translation initiation inhibitor, TdcF type

Query Match 50.0%; Score 37; DB 2; Length 128;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NNVLITDQQAQTR 15
||||| : |||
Db 40 NNVLFDADPKAQTR 53

RESULT 15
S67804
LRG1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D0764; protein YDL240w
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67804; S43158; S47956
R;Alt-Moerbe, J.; Schneider, C.; Moro, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67798
A;Accession: S67804
A;Molecule type: DNA
A;Residues: 1-1017 <ALT>
A;Cross-references: UNIPROT:P35688; UNIPARC:UPI000012E93A; EMBL:Z74288; NID:gl431407; PI
R;Muehler, A.; Xu, G.; Wells, R.; Hollenberg, C.P.; Pipersberg, W.
submitted to the EMBL Data Library, March 1994
A;Description: LRG1 is expressed during sporulation in Saccharomyces cerevisiae and cont

A;Reference number: S43158
 A;Accession: S43158
 A;Molecule type: DNA
 A;Residues: 1-530,'Q','Q',532-765,'S','S',767-790,'T',792-820,'Q',822-837,'S',839-848,'L',850-859
 A;Cross-references: UNIPARC:UPI0000168CBB; EMBL:X78453; NID:G468734; PID:G468735
 R;Mueller, L.; Xu, G.; Wells, R.; Hollenberg, C.P.; Piepersberg, W.
 Nucleic Acids Res. 22, 3151-3154, 1994
 A;Title: LRG1 is expressed during sporulation in *Saccharomyces cerevisiae* and contains m
 A;Reference number: S47956; MUID:94344779; PMID:8065929
 A;Accession: S47956
 A;Molecule type: DNA
 A;Residues: 28-89;98-136,'MF',139-148;157-184;419-474;755-765,'S',767-790,'T',792-820,'Q'
 A;Cross-references: UNIPARC:UPI000017B2C8; UNIPARC:UPI000017B2C9; UNIPARC:UPI000017B2CA;
 C;Genetics:
 A;Gene: SGD:LRG1
 A;Cross-references: SGD:S0002399; MIPS:YDL240w
 A;Map position: 4L
 C;Keywords: transmembrane protein
 F;28-89/Domain: LIM metal-binding repeat homology <LIM1>
 F;98-148/Domain: LIM metal-binding repeat homology <LIM2>
 F;157-184/Domain: LIM metal-binding repeat homology <LIM2>
 F;348-364/Domain: transmembrane #status predicted <TM1>
 F;419-474/Domain: LIM metal-binding repeat homology <LIM4>
 F;487-503/Domain: transmembrane #status predicted <TM2>

Query Match 49.3%; Score 36.5; DB 2; Length 1017;
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;
 Matches 9; Conservative 3; Mismatches 1; Indels 5; Gaps 1;
 QY 3 NVLIQTD-----QQATTR 15
 Db 583 NLVIQTDPPSSQQVSTR 600

Search completed: August 30, 2006, 04:30:57
 Job time : 9.93939 secs

This Page Blank (uspto)

```

Qy      1 RNNVLQTDOQATTR 15
      :|:|:|:|:|:|:
Db      1302 KNEILMQADSQATTQ 1316

RESULT 2
Q92WJ7 RHIME
ID Q92WJ7 RHIME PRELIMINARY; PRT; 917 AA.
AC Q92WJ7;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Putative sensory histidine kinase protein.

```


RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loulseghe H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzner M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuapa A.;
RT "The genome of the social amoeba *Dictyostelium discoideum*.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBS whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AAF10100013; EAL11869.1; -; Genomic_DNA.
DR KW Hypothetical protein.
SQ SEQUENCE 649 AA; 77580 MW; B366AD152ACDDA23 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 649;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQQT 14
Db 611 NNVLITDQQT 623

RESULT 5
Q9HRN4 HALSA
ID O9HRN4 HALSA PRELIMINARY; PRT; 285 AA..
AC O9HRN4;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Vng0617h.
GN OrderedLocusNames=VNG0617H;
OS Halobacterium salinarum (Halobacterium halobium).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Laaky S.R., Baliga N.S., Thorsson V., Shrogha J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlshocher M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of *Halobacterium* species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AE005010; AAG19124.1; -; Genomic_DNA.
DR PIR; H84219; H84219.
DR BioCyc; HSP64091:VNG0617H-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 285 AA; 29163 MW; 31223D1A949BC1B3 CRC64;

Query Match 58.8%; Score 43.5; DB 2; Length 285;
Best Local Similarity 58.8%; Pred. No. 15;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 2 NNVLITDQQT---ATTR 15
Db 212 NNVLITDQDSELTTR 228

RESULT 6
Q5C614 SCHJA
ID Q5C614 SCHJA PRELIMINARY; PRT; 161 AA.
AC Q5C614;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 2.
DT 07-FEB-2006, entry version 5.
DE SUCHG07893 protein (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Pigenea; Strigeidida;
OC Schistosomatida; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
RA Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
RA Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
RA Han Z.-G.;
RT "New Perspectives on Host-parasite Interplay by Comparative
RT Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
RT Schistosoma japonicum.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AY808851; AAX24740.2; -; mRNA.
DR NON TER 161
SQ SEQUENCE 161 AA; 18352 MW; 1A6BF6544526AE04 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 161;
Best Local Similarity 57.1%; Pred. No. 9.9;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQQT 15
Db 84 NNVLITDQQT 97

RESULT 7
Q5WV87 LEGPL
ID Q5WV87 LEGPL PRELIMINARY; PRT; 416 AA.
AC Q5WV87;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
GN OrderedLocusNames=lp11930;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the *Legionella pneumophila* genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CR628337; CAH16170.1; -; Genomic_DNA.
DR Legioliist; lp11930; -.
KW Complete proteome; Hypothetical protein.

```
SQ SEQUENCE 416 AA; 48862 MW; OE153EDD3778559E CRC64;
Query Match 58.1%; Score 43; DB 2; Length 416;
Best Local Similarity 69.2%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLITDQQATT 14
||||| :|||
Db 63 NNVLIPLEQQPTT 75

RESULT 8
Q5X3U5_LEGPA
ID Q5X3U5_LEGPA PRELIMINARY; PRT; 417 AA.
AC Q5X3U5;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Hypothetical protein.
GN OrderedLocusNames=lp1939;
OS Legionella pneumophila (strain Paris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazale C., Rusnik C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glauser P., Buchrieser C.;
DE "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR628336; CAH13091.1; -; Genomic_DNA.
KW Legiolysin; lpp1939; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 417 AA; 49131 MW; 01F68A54B430C7E2 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 417;
Best Local Similarity 69.2%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLITDQQATT 14
||||| :|||
Db 63 NNVLIPLEQQPTT 75

RESULT 9
Q5ZU51_LEGPH
ID Q5ZU51_LEGPH PRELIMINARY; PRT; 463 AA.
AC Q5ZU51;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE EhaA protein.
GN OrderedLocusNames=lp91957;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
OS ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamari G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Steshenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
```

```
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila.";
RL Science 305:1966-1968(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE017354; AAU28026.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 463 AA; 54449 MW; BE76CBED5D81D264 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 463;
Best Local Similarity 69.2%; Pred. No. 34;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLITDQQATT 14
||||| :|||
Db 87 NNVLIPLEQQPTT 99

RESULT 10
Q7R036_GIALA
ID Q7R036_GIALA PRELIMINARY; PRT; 505 AA.
AC Q7R036;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE GIP 456 18539 20056.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AACB01000038; EAA40651.1; -; Genomic_DNA.
DR InterPro; IPR003198; Amidino trans.
DR Pfam; PF02274; Amidinotransf; 1.
SQ SEQUENCE 505 AA; 55735 MW; 99E2CBF5B56824B0 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 505;
Best Local Similarity 57.1%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLITDQQATT 15
||||| :|||
Db 93 NNWFMEDQQITTR 106

RESULT 11
Q27657_GIALA
ID Q27657_GIALA PRELIMINARY; PRT; 580 AA.
AC Q27657;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Arginine deiminase (EC 3.5.3.6).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
```

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Portland 1;
 RX MEDLINE=98136144; PubMed=9468500; DOI=10.1074/jbc.273.8.4470;
 RA Knodler L.A., Sekyere E.O., Stewart T.S., Schofield P.J.,
 RA Edwards M.R.;
 RT Cloning and expression of a prokaryotic enzyme, arginine deiminase,
 RT from a primitive eukaryote *Giardia intestinalis*.
 RL J. Biol. Chem. 273:4470-4477(1998).
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: U49236; AAC06116.1; -; Genomic_DNA.
 DR PIR: T45064.
 DR BioCyc: MetaCyc:MONOMER-11205; -.
 DR GO: GO:0016990; F:arginine deiminase activity; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR InterPro: IPR003198; Amidino trans.
 DR Pfam: PF02274; Amidinotransf_1.
 KW Hydrolase.
 SQ SEQUENCE 580 AA; 64132 MW; 4812F389D0F5357A CRC64;
 Query Match 58.1%; Score 43; DB 2; Length 580;
 Best Local Similarity 57.1%; Pred. No. 44;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 NNVLQTDQOATTR 15
 DB 168 NNVFMEDQITTR 181
 RESULT 12
 ID Q7ZXI4 XENLA PRELIMINARY; PRT; 854 AA.
 AC Q7ZXI4;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 20.
 DE MGC52979 protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative".
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the AAA ATPase family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: BC044980; AAH44980.1; -; mRNA.
 DR HSSP: Q01853; IR7R.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0017111; F:nucleoside-triphosphatase activity; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003959; AAA_ATPase_cent.
 DR InterPro: IPR003960; AAA_sub.
 DR Pfam: PF00004; AAA; 2.
 DR SMART: SM00382; AAA; 2.
 DR PROSITE: PS00674; AAA; 2.
 KW ATP-binding; Nucleotide-binding.
 SQ SEQUENCE 854 AA; 93597 MW; F91339E502C41B3 CRC64;
 Query Match 56.1%; Score 41.5; DB 2; Length 854;
 Best Local Similarity 78.6%; Pred. No. 1.4e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 2 NNVLQ-TDQOATT 14
 DB 483 NRVLQIKDQOATT 496
 RESULT 13
 ID Q8H475 ORYSA PRELIMINARY; PRT; 106 AA.
 AC Q8H475;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Hypothetical protein P0470D12.115.
 GN Name=P0470D12.115;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Ehrhartoideae; Oryzoideae; Oryzae;
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
 RT clone:P0470D12".
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: AP004300; BAC15985.1; -; Genomic_DNA.
 DR Gramene; Q8H475; -.
 KW Hypothetical protein.
 SQ SEQUENCE 106 AA; 12281 MW; 8016731B1945298F CRC64;
 Query Match 55.4%; Score 41; DB 2; Length 106;
 Best Local Similarity 46.7%; Pred. No. 15;
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RNNVLQTDQOATTR 15
 DB 10 RNNGVMELEQATSR 24

```

RESULT 14
Q6FP28_CANGA
ID Q6FP28_CANGA PRELIMINARY; PRT; 247 AA.
AC Q6FP28;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Similar to sp|P39721 Saccharomyces cerevisiae YAL049C.
GN OrderedLocusNames=CAGL0J071283;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OK NCBI_TaxID=5478;
RN [1]
FN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Bolesame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniun-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
FT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CR380956; CAG60967.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002925; DieneLactn_hydro.
DR Pfam; PF01738; DLH; 1.
KW Complete proteome.
SQ SEQUENCE 247 AA; 27274 MW; AEB540BB8B628D35 CRC64;

Query Match 55.4%; Score 41; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIQTDQAT 13
Db 57 NNVLITADQMAT 68

RESULT 15
Q4SVF5_TETNG
ID Q4SVF5_TETNG PRELIMINARY; PRT; 260 AA.
AC Q4SVF5;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chromosome 7 SCF13760, whole genome shotgun sequence.
GN ORFNames=GSTEN00012005001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OK NCBI_TaxID=99883;
RN [1]
FN NUCLEOTIDE SEQUENCE.
RP PubMed=15496914; DOI=10.1038/nature03025;
RX PubMed=15496914; DOI=10.1038/nature03025;

Query Match 55.4%; Score 41; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIQTDQAT 13
Db 57 NNVLITADQMAT 68

Search completed: August 30, 2006, 04:29:21
Job time : 61.4848 secs

```

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	43	58.1	580	2	US-09-723-546-10	Sequence 10, Appl	
2	41	55.4	108	2	US-09-281-760B-37	Sequence 37, Appl	
3	41	55.4	312	2	US-09-701-623C-2	Sequence 2, Appl	
4	41	55.4	426	1	US-08-336-583-2	Sequence 2, Appl	
5	41	55.4	426	5	PCT-US95-13795-2	Sequence 2, Appl	
6	38	51.4	345	2	US-09-270-767-41480	Sequence 41480, A	
7	38	51.4	613	2	US-09-026-001A-10	Sequence 10, Appl	
8	38	51.4	613	2	US-09-596-620-10	Sequence 10, Appl	
9	38	51.4	621	2	US-09-026-001A-18	Sequence 18, Appl	
10	38	51.4	621	2	US-09-596-620-18	Sequence 18, Appl	
11	37	50.0	370	2	US-09-328-352-5826	Sequence 5826, Ap	
12	37	50.0	431	2	US-09-479-614-14	Sequence 14, Appl	
13	37	50.0	436	2	US-09-479-614-2	Sequence 2, Appl	
14	37	50.0	436	2	US-09-479-614-29	Sequence 29, Appl	
15	36	48.6	153	2	US-09-348-796A-22386	Sequence 22386, A	
16	36	48.6	199	2	US-09-107-433-2754	Sequence 2754, Ap	
17	36	48.6	383	2	US-09-328-352-5969	Sequence 5969, Ap	
18	36	48.6	441	2	US-08-583-110-4400	Sequence 4400, Ap	
19	36	48.6	445	2	US-09-107-433-5039	Sequence 5039, Ap	
20	36	48.6	447	2	US-09-205-258-408	Sequence 408, App	
21	36	48.6	447	2	US-10-004-860-408	Sequence 408, App	
22	36	48.6	461	2	US-09-591-181-301	Sequence 301, App	
23	36	48.6	461	2	US-09-590-444-301	Sequence 301, App	
24	36	48.6	461	2	US-09-597-333-301	Sequence 301, App	
25	36	48.6	461	2	US-09-592-598-301	Sequence 301, App	
26	36	48.6	461	2	US-09-589-735-301	Sequence 301, App	

```
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (460)..(462)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (530)..(530)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (568)..(568)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (847)..(849)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (853)..(853)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1382)..(1382)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1832)..(1832)
; OTHER INFORMATION: "n" stands for any nucleic acid
; US-09-281-760E-37
```

```
Query Match          55.4%; Score 41; DB 2; Length 108;
Best Local Similarity 64.3%; Pred. No. 4.7;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 RNNVLIQTDOQATT 14
Db 43 RNDSPIQTDQYTTT 56
```

```
RESULT 3
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153U51
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRI
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2
```

```
Query Match          55.4%; Score 41; DB 2; Length 312;
Best Local Similarity 64.3%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 RNNVLIQTDOQATT 14
Db 255 RNDSPIQTDQYTTT 268
```

```
RESULT 4
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2
```

```
Query Match          55.4%; Score 41; DB 1; Length 426;
Best Local Similarity 64.3%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 RNNVLIQTDOQATT 14
Db 357 RNDSPIQTDQYTTT 370
```

RESULT 5
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 55.4%; Score 41; DB 5; Length 426;
Best Local Similarity 64.3%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14
||:|||||
Db 357 RNDSPITQDQYTT 370

RESULT 6
US-09-270-767-41480
; Sequence 41480, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41480
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41480

Query Match 51.4%; Score 38; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 63;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 RNNVLIQTDDQATT 15
||:|||||
Db 77 NQKLIRKNOQTTR 90

RESULT 7
US-09-026-001A-10
; Sequence 10, Application US/09026001A
; Patent No. 6413760
; GENERAL INFORMATION:
; APPLICANT: Boodhoo, Amechand
; APPLICANT: Seehra, Jasbir
; APPLICANT: Shaw, Gray
; APPLICANT: Sako, Dianne
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,001A
; FILING DATE: 18-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 613 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-026-001A-10

Query Match 51.4%; Score 38; DB 2; Length 613;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQAT 13
||:|||||
Db 261 RNEINVQSDVQAT 273

RESULT 8
US-09-996-620-10
; Sequence 10, Application US/09996620
; Patent No. 6881404
; GENERAL INFORMATION:
; APPLICANT: Boodhoo, Amechand
; APPLICANT: Seehra, Jasbir
; APPLICANT: Shaw, Gray
; APPLICANT: Sako, Dianne
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
; PROTEASE, POLYNUCLEOTIDES ENCODING SAME AND RELATED PROTEAS
; THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,620
FILING DATE: 27-NO. 6881404-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,001
FILING DATE: 18-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-996-620-10

Query Match 51.4%; Score 38; DB 2; Length 613;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQAT 13
||:|:|:|
DB 261 RNEINVQSDVQAT 273

RESULT 9
US-09-026-001A-18
Sequence 18, Application US/09026001A
Patent No. 6413760
GENERAL INFORMATION:
APPLICANT: Boodhoo, Amechand
APPLICANT: Seehra, Jasbir
APPLICANT: Shaw, Gray
APPLICANT: Sako, Dianne
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 621 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-026-001A-18

Query Match 51.4%; Score 38; DB 2; Length 621;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQAT 13
||:|:|:|
DB 269 RNEINVQSDVQAT 281

RESULT 10
US-09-996-620-18
Sequence 18, Application US/09996620
Patent No. 6881404
GENERAL INFORMATION:
APPLICANT: Boodhoo, Amechand
APPLICANT: Seehra, Jasbir
APPLICANT: Shaw, Gray
APPLICANT: Sako, Dianne
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: THERAPEUTIC USES THEREOF

Query Match 51.4%; Score 38; DB 2; Length 613;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQAT 13
||:|:|:|
DB 261 RNEINVQSDVQAT 273

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,620
FILING DATE: 27-NO. 6881404-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,001
FILING DATE: 18-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 621 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-996-620-18

Query Match 51.4%; Score 38; DB 2; Length 621;

```
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 13
   ||:|:|:|
Db 269 RNEINVQSDVQAT 281

RESULT 11
US-09-328-352-5826
; Sequence 5826, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5826
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5826

Query Match 50.0%; Score 37; DB 2; Length 370;
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14
   :||::||:|
Db 175 KNNIVYTTDSATS 188

RESULT 12
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 50.0%; Score 37; DB 2; Length 431;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLITDQQT 14
   |:|:|:|
Db 363 NDSFVRTEQQATT 375

RESULT 13
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
```

```
FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 50.0%; Score 37; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLITDQQT 14
   |:|:|:|
Db 428 NDSFVRTEQQATT 440

RESULT 14
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 50.0%; Score 37; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLITDQQT 14
   |:|:|:|
Db 428 NDSFVRTEQQATT 440

RESULT 15
US-09-248-796A-22386
; Sequence 22386, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22386
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22386
```

Query Match 48.6%; Score 36; DB 2; Length 153;
Best Local Similarity 77.8%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNNVLIQTD 9
||| |||
Db 21 RNNYFIQTD 29

Search completed: August 30, 2006, 04:33:03
Job time : 15.8485 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 75.7576 Seconds
(without alignments)
91.717 Million cell updates/sec

Title: US-10-758-165a-3

Perfect score: 74

Sequence: 1 RNNVLIQTDDQATTR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.Main.*

1: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SID3S/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	US-10-758-165-3	Sequence 3, Appli
2	74	100.0	424	US-10-451-078-2	Sequence 2, Appli
3	74	100.0	424	US-10-451-078-4	Sequence 4, Appli
4	74	100.0	569	US-10-214-524-30	Sequence 30, Appli
5	49	66.2	15	US-10-052-788-4	Sequence 4, Appli
6	43	58.1	580	US-10-674-666-17	Sequence 17, Appli
7	43	58.1	580	US-10-757-843-10	Sequence 10, Appli
8	41.5	56.1	854	US-10-732-923-23294	Sequence 23294, A
9	41	55.4	15	US-10-758-165-1	Sequence 1, Appli
10	41	55.4	105	US-10-437-963-129557	Sequence 129557,
11	41	55.4	312	US-10-369-493-6713	Sequence 6713, Ap
12	41	55.4	312	US-10-723-207-2	Sequence 2, Appli
13	41	55.4	426	US-10-214-524-28	Sequence 28, Appli
14	41	55.4	917	US-10-437-963-181484	Sequence 181484,
15	40	54.1	15	US-10-758-165-7	Sequence 7, Appli
16	40	54.1	567	US-10-214-524-33	Sequence 33, Appli
17	38	51.4	558	US-10-437-963-185049	Sequence 185049,
18	38	51.4	613	US-09-996-620-10	Sequence 10, Appli
19	38	51.4	613	US-11-066-236-10	Sequence 10, Appli
20	38	51.4	621	US-09-996-620-18	Sequence 18, Appli
21	38	51.4	621	US-11-066-236-18	Sequence 18, Appli
22	38	51.4	703	US-10-282-122A-72382	Sequence 72382, A
23	38	51.4	814	US-10-128-714-8100	Sequence 8100, Ap
24	38	51.4	902	US-11-188-298-12745	Sequence 12745, A
25	38	51.4	1827	US-11-057-058-62	Sequence 62, Appli
26	37	50.0	15	US-10-758-165-2	Sequence 2, Appli
27	37	50.0	67	US-10-437-963-138338	Sequence 138338,

28 37 50.0 223 4 US-10-389-566-587 Sequence 587, Appli
29 37 50.0 431 3 US-09-479-614-14 Sequence 14, Appli
30 37 50.0 431 4 US-10-409-772-14 Sequence 14, Appli
31 37 50.0 496 3 US-09-479-614-2 Sequence 2, Appli
32 37 50.0 496 3 US-09-479-614-29 Sequence 29, Appli
33 37 50.0 496 4 US-10-214-524-25 Sequence 25, Appli
34 37 50.0 496 4 US-10-409-772-2 Sequence 2, Appli
35 37 50.0 496 4 US-10-409-772-29 Sequence 29, Appli
36 37 50.0 663 4 US-10-389-566-1053 Sequence 1053, Ap
37 37 50.0 663 5 US-10-732-923-9730 Sequence 9730, Ap
38 37 50.0 750 4 US-10-425-115-351098 Sequence 351098,
39 36.5 49.3 272 4 US-10-425-115-233903 Sequence 233903,
40 36 48.6 21 4 US-10-340-288-37 Sequence 37, Appli
41 36 48.6 143 4 US-10-128-714-8304 Sequence 8304, Ap
42 36 48.6 199 4 US-10-425-115-299967 Sequence 299967,
43 36 48.6 199 5 US-10-617-320-2754 Sequence 2754, Ap
44 36 48.6 309 4 US-10-264-237-2751 Sequence 2751, Ap
45 36 48.6 318 4 US-10-128-714-3304 Sequence 3304, Ap

ALIGNMENTS

RESULT 1

US-10-758-165-3

; Sequence 3, Application US/10758165

; Publication No. US20050196816A1

; GENERAL INFORMATION:

; APPLICANT: Hammerberg, Bruce

; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

; FILE REFERENCE: 5051-661

; CURRENT APPLICATION NUMBER: US/10758,165

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: US 60/440,472

; PRIOR FILING DATE: 2003-01-16

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Equus caballus

US-10-758-165-3

Query Match 100.0%; Score 74; DB 5; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15

Db 1 RNNVLIQTDDQATTR 15

RESULT 2

US-10-451-078-2

; Sequence 2, Application US/10451078

; Publication No. US20040115764A1

; GENERAL INFORMATION:

; APPLICANT: Leibold, Wolfgang

; APPLICANT: Bettina, Wagner

; APPLICANT: Radbruch, Andreas

; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the Heavy Chain of an Equine IGE Allotype, Recombinant

; TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding

; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use

; FILE REFERENCE: 03100177aa

; CURRENT APPLICATION NUMBER: US/10/451,078

; CURRENT FILING DATE: 2003-12-24

; PRIOR APPLICATION NUMBER: PCT/DE01/04810

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: DE 100 64 415.5

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Equus caballus
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (1)..(97)
; OTHER INFORMATION: CH1 domain, IgE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (98)..(205)
; OTHER INFORMATION: CH2 domain, IgE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (206)..(312)
; OTHER INFORMATION: CH3 domain, IgE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (313)..(424)
; OTHER INFORMATION: CH4 domain, IgE allotype a
; US-10-451-078-2

Query Match      100.0%; Score 74; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
Db 356 RNNVLIQTDDQATTR 370

RESULT 3
US-10-451-078-4
; Sequence 4, Application US/10451078
; Publication No. US20040115764A1
; GENERAL INFORMATION:
; APPLICANT: Leibold, Wolfgang
; APPLICANT: Bettina, Wagner
; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
; TITLE OF INVENTION: Heavy Chain of an Equine IgE Allotype, Recombinant
; TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
; FILE REFERENCE: 03100177aa
; CURRENT APPLICATION NUMBER: US/10/451.078
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: PCT/DE01/04810
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Equus caballus
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (1)..(97)
; OTHER INFORMATION: CH1 domain, IgE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (98)..(205)
; OTHER INFORMATION: CH2 domain, IgE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (206)..(312)
; OTHER INFORMATION: CH3 domain, IgE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (313)..(424)
; OTHER INFORMATION: CH4 domain, IgE allotype b
; US-10-451-078-4
```

```
Query Match      100.0%; Score 74; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
Db 356 RNNVLIQTDDQATTR 370

RESULT 4
US-10-214-524-30
; Sequence 30, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214.524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Horse (Equus caballus)
; US-10-214-524-30
```

```
Query Match      100.0%; Score 74; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
Db 501 RNNVLIQTDDQATTR 515

RESULT 5
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; TITLE OF INVENTION: Induction of Anti-IgE Antibodies
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052.788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide
; OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon
; OTHER INFORMATION: heavy chain
; US-10-052-788-4
```

```
Query Match      66.2%; Score 49; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IQTDQATTR 15
```

Db 1 IOTDQQATTR 10
|||||

RESULT 6
US-10-674-666-17
; Sequence 17, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-674-666-17

Query Match 58.1%; Score 43; DB 4; Length 580;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLQTDQQATTR 15
||: ||| |||

Db 168 NNVFMRDQOITR 181

RESULT 7
US-10-757-843-10
; Sequence 10, Application US/10757843
; Publication No. US20050129706A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0059
; CURRENT APPLICATION NUMBER: US/10/757,843
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/723,546
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 10
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-757-843-10

Query Match 58.1%; Score 43; DB 5; Length 580;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLQTDQQATTR 15
||: ||| |||

Db 168 NNVFMRDQOITR 181

RESULT 8
US-10-732-923-23294
; Sequence 23294, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 23294
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-732-923-23294

Query Match 56.1%; Score 41.5; DB 5; Length 854;
Best Local Similarity 78.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2 NNVLQTDQQATTR 14
| ||| ||| |||

Db 483 NRVLQIKDQQATT 496

RESULT 9
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match 55.4%; Score 41; DB 5; Length 15;
Best Local Similarity 64.3%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLQTDQQATT 14
||: ||| |||

Db 1 RNDSPITDQYTTT 14

RESULT 10
US-10-437-963-129557
; Sequence 129557, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 129557
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31803C.1.pep

US-10-437-963-129557
; Sequence 129557, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 129557
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31803C.1.pep

US-10-437-963-129557

Query Match 55.4%; Score 41; DB 4; Length 105;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTR 15
|||:::|||||
Db 10 RNNGVMELEQATSR 24

RESULT 11

US-10-369-493-6713

; Sequence 6713, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 6713

; LENGTH: 312

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-6713

Query Match 55.4%; Score 41; DB 4; Length 312;
Best Local Similarity 57.1%; Pred. No. 67;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLITDQDQATTR 15
:|||||:|:
Db 159 DNVLQKDEENTAR 172

RESULT 12

US-10-723-207-2

; Sequence 2, Application US/10723207

; Publication No. US20050250934A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; APPLICANT: Walfield, Alan M.

; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

; FILE REFERENCE: 1151-41530S2

; CURRENT APPLICATION NUMBER: US/10/723,207

; CURRENT FILING DATE: 2003-11-24

; PRIOR APPLICATION NUMBER: 09/701,623

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: PCT/US99/13959

; PRIOR FILING DATE: 1999-06-21

; PRIOR APPLICATION NUMBER: 09/100,287

; PRIOR FILING DATE: 1998-06-20

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 312

; TYPE: PRT

; ORGANISM: Dog

; FEATURE:

; OTHER INFORMATION: CH2CH3n of dog IgE

; PUBLICATION INFORMATION:

; AUTHORS: Patel,

; JOURNAL: Immunogenetics

; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2

Query Match 55.4%; Score 41; DB 5; Length 312;
Best Local Similarity 64.3%; Pred. No. 67;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTT 14
||:|||||
Db 255 RNDSPITDQYTTT 268

RESULT 13

US-10-214-524-28

; Sequence 28, Application US/10214524

; Publication No. US20030073142A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Swei-Shen Alex

; APPLICANT: Yang, Yong-Min

; APPLICANT: Barankiewicz, Theresa J.

; APPLICANT: Chen, Zhong

; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF

; FILE REFERENCE: ICE-00101.P.1-1

; CURRENT APPLICATION NUMBER: US/10/214,524

; CURRENT FILING DATE: 2002-08-08

; PRIOR APPLICATION NUMBER: 60/312,120

; PRIOR FILING DATE: 2001-08-13

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 28

; LENGTH: 426

; TYPE: PRT

; ORGANISM: Dog (Canis familiaris)

US-10-214-524-28

Query Match 55.4%; Score 41; DB 4; Length 426;
Best Local Similarity 64.3%; Pred. No. 95;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATTT 14
||:|||||
Db 357 RNDSPITDQYTTT 370

RESULT 14

US-10-437-963-181484

; Sequence 181484, Application US/10437963.

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 181484

; LENGTH: 917

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(917)

; OTHER INFORMATION: unsure at all Xaa locations

```
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78753C.1.pep
US-10-437-963-181484

Query Match      55.4%; Score 41; DB 4; Length 917;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14
Db 143 RNNIMVILDNQMTT 156

RESULT 15
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: S051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match      54.1%; Score 40; DB 5; Length 15;
Best Local Similarity 46.7%; Pred. No. 3.3;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 15
Db 1 RNDAPVQADRHSTTR 15
```

Search completed: August 30, 2006, 05:13:02
Job time : 76.7576 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 7.72727 Seconds
(without alignments)
133.695 Million cell updates/sec

Title: US-10-758-165a-3

Perfect score: 74

Sequence: 1 RNNVLIQTDDQATT 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SIDS3/prodata/1/pubpa/US09_NEW_PUB.psp.*
- 2: /EMC_Celerra_SIDS3/prodata/1/pubpa/US06_NEW_PUB.psp.*
- 3: /EMC_Celerra_SIDS3/prodata/1/pubpa/US07_NEW_PUB.psp.*
- 4: /EMC_Celerra_SIDS3/prodata/1/pubpa/US08_NEW_PUB.psp.*
- 5: /EMC_Celerra_SIDS3/prodata/1/pubpa/PCT_NEW_PUB.psp.*
- 6: /EMC_Celerra_SIDS3/prodata/1/pubpa/US10_NEW_PUB.psp.*
- 7: /EMC_Celerra_SIDS3/prodata/1/pubpa/US11_NEW_PUB.psp.*
- 8: /EMC_Celerra_SIDS3/prodata/1/pubpa/US60_NEW_PUB.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	51.4	554	6	US-10-449-902-40987 Sequence 40987, A
2	36	48.6	348	7	US-11-197-712-247 Sequence 247, App
3	36	48.6	585	7	US-11-330-403-2292 Sequence 2292, App
4	35	47.3	223	6	US-10-953-349-1194 Sequence 1194, App
5	35	47.3	223	7	US-11-056-355B-23703 Sequence 23703, A
6	35	47.3	240	6	US-10-953-349-1098 Sequence 1098, App
7	35	47.3	240	7	US-11-056-355B-43157 Sequence 43157, A
8	35	47.3	240	7	US-11-056-355B-85177 Sequence 85177, A
9	35	47.3	317	6	US-10-953-349-1193 Sequence 1193, App
10	35	47.3	317	7	US-11-056-355B-23702 Sequence 23702, A
11	35	47.3	388	6	US-10-953-349-1192 Sequence 1192, App
12	35	47.3	388	7	US-11-056-355B-23701 Sequence 23701, A
13	35	47.3	409	6	US-10-953-349-1097 Sequence 1097, App
14	35	47.3	409	7	US-11-056-355B-43156 Sequence 43156, A
15	35	47.3	409	7	US-11-056-355B-85176 Sequence 85176, A
16	35	47.3	498	6	US-10-953-349-37842 Sequence 37842, A
17	35	47.3	578	6	US-10-953-349-37841 Sequence 37841, A
18	35	47.3	634	6	US-10-953-349-37840 Sequence 37840, A
19	35	47.3	825	7	US-11-330-403-2887 Sequence 2887, App
20	34	45.9	257	7	US-11-056-355B-18603 Sequence 18603, A
21	34	45.9	358	6	US-10-953-349-4802 Sequence 4802, App
22	34	45.9	358	7	US-11-056-355B-27751 Sequence 27751, A
23	34	45.9	358	7	US-11-056-355B-31341 Sequence 31341, A
24	34	45.9	358	7	US-11-056-355B-105308 Sequence 105308, A
25	34	45.9	358	7	US-11-056-355B-116547 Sequence 116547, A

ALIGNMENTS

RESULT 1

US-10-449-902-40987
; Sequence 40987, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40987
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-40987

Query Match 51.4% Score 38; DB 6; Length 554;
Best Local Similarity 42.9% Pred. No. 30;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDDQATT 14
Db 144 KNNIMVLDNQMTT 157

RESULT 2

US-11-197-712-247
; Sequence 247, Application US/11197712
; Publication No. US20060130160A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US4 CIP
; CURRENT APPLICATION NUMBER: US/11/197,712
; PRIOR FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/03/876,997
; PRIOR FILING DATE: 2001-06-08

Sequence 71337, A
Sequence 71336, A
Sequence 2882, App
Sequence 69409, A
Sequence 69694, A
Sequence 71537, A
Sequence 86118, A
Sequence 69408, A
Sequence 71335, A
Sequence 69693, A
Sequence 72244, A
Sequence 71536, A
Sequence 86117, A
Sequence 72243, A
Sequence 69407, A
Sequence 72242, A
Sequence 3735, App
Sequence 17556, A
Sequence 71535, A
Sequence 86116, A

; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 247
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -29...-1
US-11-197-712-247

Query Match 48.6%; Score 36; DB 7; Length 348;
Best Local Similarity 53.8%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 NVLIQTQQATFR 15
|||::|||
Db 175 NVVETDQIMVR 187

RESULT 3

US-11-330-403-2292
; Sequence 2292, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 2292
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15
US-11-330-403-2292

Query Match 48.6%; Score 36; DB 7; Length 585;
Best Local Similarity 75.0%; Pred. No. 77;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NNVLQT D 9
|||::|||
Db 243 NNVLVETD 250

RESULT 4

US-10-953-349-1194
; Sequence 1194, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1194
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1194

Query Match 47.3%; Score 35; DB 6; Length 223;
Best Local Similarity 50.0%; Pred. No. 39;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RNNVLIQTQQATT 14
|||::|||
Db 195 RQNVVVELVQAATT 208

RESULT 5

US-11-056-355B-23703
; Sequence 23703, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 23703
; LENGTH: 223
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(223)
; OTHER INFORMATION: Ceres Seq. ID no. 13487886
US-11-056-355B-23703

Query Match 47.3%; Score 35; DB 7; Length 223;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTQQATT 14
|||::|||
Db 195 RQNVVVELVQAATT 208

RESULT 6

US-10-953-349-1098
; Sequence 1098, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1098
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1098

Query Match 47.3%; Score 35; DB 6; Length 240;
Best Local Similarity 38.5%; Pred. No. 42;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLQTQQATT 14
|||::|||
Db 11 NNVLKLDQASTS 23

RESULT 7

US-11-056-355B-43157
; Sequence 43157, Application US/11056355B
; Publication No. US20060150283A1

```
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 43157
; LENGTH: 240
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(240)
; OTHER INFORMATION: Ceres Seq. ID no. 13487787
US-11-056-355B-43157

Query Match      47.3%; Score 35; DB 7; Length 240;
Best Local Similarity 38.5%; Pred. No. 42;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      2 NNVLQTDQQAATT 14
Db      11 NNVLKLDQASTS 23

RESULT 8
US-11-056-355B-85177
; Sequence 85177, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 85177
; LENGTH: 240
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(240)
; OTHER INFORMATION: Ceres Seq. ID no. 12679238
US-11-056-355B-85177

Query Match      47.3%; Score 35; DB 7; Length 240;
Best Local Similarity 38.5%; Pred. No. 42;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      2 NNVLQTDQQAATT 14
Db      11 NNVLKLDQASTS 23

RESULT 9
US-10-953-349-1193
; Sequence 1193, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
```

```
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1193
; LENGTH: 317
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1193

Query Match      47.3%; Score 35; DB 6; Length 317;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLQTDQQAATT 14
Db      289 RQNVVVELVQAATT 302

RESULT 10
US-11-056-355B-23702
; Sequence 23702, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 23702
; LENGTH: 317
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(317)
; OTHER INFORMATION: Ceres Seq. ID no. 13487885
US-11-056-355B-23702

Query Match      47.3%; Score 35; DB 7; Length 317;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLQTDQQAATT 14
Db      289 RQNVVVELVQAATT 302

RESULT 11
US-10-953-349-1192
; Sequence 1192, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1192
; LENGTH: 388
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1192

Query Match      47.3%; Score 35; DB 6; Length 388;
```

Best Local Similarity 50.0%; Pred. No. 74;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLQTDQQAATT 14
| | | | |
Db 360 RQNVVVELVQAATT 373

RESULT 12

US-11-056-355B-23701
; Sequence 23701, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 23701
; LENGTH: 388
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(388)
; OTHER INFORMATION: Ceres Seq. ID no. 13487884
US-11-056-355B-23701

Query Match 47.3%; Score 35; DB 7; Length 388;
Best Local Similarity 50.0%; Pred. No. 74;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLQTDQQAATT 14
| | | | |
Db 360 RQNVVVELVQAATT 373

RESULT 13

US-10-953-349-1097
; Sequence 1097, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1097
; LENGTH: 409
; TYPE: PRP
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1097

Query Match 47.3%; Score 35; DB 6; Length 409;
Best Local Similarity 38.5%; Pred. No. 79;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RNNVLQTDQQAATT 14
| | | | |
Db 180 RNNVLKLDQAATS 192

RESULT 14

US-11-056-355B-43156
; Sequence 43156, Application US/11056355B

Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 43156
; LENGTH: 409
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(409)
; OTHER INFORMATION: Ceres Seq. ID no. 13487786
US-11-056-355B-43156

Query Match 47.3%; Score 35; DB 7; Length 409;
Best Local Similarity 38.5%; Pred. No. 79;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RNNVLQTDQQAATT 14
| | | | |
Db 180 RNNVLKLDQAATS 192

RESULT 15

US-11-056-355B-85176
; Sequence 85176, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 85176
; LENGTH: 409
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(409)
; OTHER INFORMATION: Ceres Seq. ID no. 12679237
US-11-056-355B-85176

Query Match 47.3%; Score 35; DB 7; Length 409;
Best Local Similarity 38.5%; Pred. No. 79;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RNNVLQTDQQAATT 14
| | | | |
Db 180 RNNVLKLDQAATS 192

Search completed: August 30, 2006, 04:35:58
Job time : 7.72727 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 65.4545 Seconds
(without alignments)
125.735 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97

Sequence: 1 VDGQKATNIPFYTAPGK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	ADRI0609	Dog IgE e
2	97	100.0	312	AAY79995	Dog immun
3	97	100.0	417	AAW23067	Canine Ig
4	97	100.0	426	AAR97753	Canine Ig
5	97	100.0	426	ABP96583	Dog IgE h
6	87	89.7	18	ADRI0610	Cat IgE e
7	87	89.7	431	ADG73237	Cat immun
8	87	89.7	496	ABP96580	Cat IgE h
9	87	89.7	496	ABU09338	Feline Ig
10	87	89.7	496	ABU09336	Feline Ig
11	87	89.7	496	ADG73251	Cat parti
12	87	89.7	496	ADG73225	Cat parti
13	73	75.3	577	ABP96584	Duckbille
14	68	70.1	343	AA06204	Platypus
15	58	59.8	337	ADP90022	Opussum-r
16	58	59.8	337	ADN00643	ORO prote
17	58	59.8	338	ADP90025	Opussum-h
18	58	59.8	338	ADN00646	OSO prote
19	58	59.8	341	ABP96206	Immunogen
20	58	59.8	341	AA03644	Opussum I
21	58	59.8	341	AA06208	Immunogen
22	58	59.8	342	AA06205	Immunogen
23	58	59.8	345	AA06207	Immunogen

24	58	59.8	347	8	ADF90033	Adf90033	Opussum-h
25	58	59.8	347	8	ADN00654	Adn00654	OSO-H pro
26	58	59.8	353	8	ADN00661	Adn00661	H-OCO-H p
27	58	59.8	427	6	ABP96591	Abp96591	Brushtail
28	58	59.8	446	6	ABP96587	Abp96587	Opussum I
29	58	59.8	555	8	ADP90027	Adp90027	Opussum-r
30	58	59.8	555	8	ADN00648	Adn00648	ORORO pro
31	58	59.8	557	8	ADF90031	Adf90031	Opussum-h
32	58	59.8	557	8	ADF90035	Adf90035	Opussum-h
33	58	59.8	557	8	ADN00656	Adn00656	OSO pro
34	58	59.8	557	8	ADN00652	Adn00652	modOSO
35	58	59.8	566	8	ADP90029	Adp90029	Opussum-h
36	58	59.8	566	8	ADF90037	Adf90037	Opussum-h
37	58	59.8	566	8	ADN00658	Adn00658	OSO-H p
38	58	59.8	566	8	ADN00650	Adn00650	modOSO
39	55	56.7	18	8	ADRI0612	Adri0612	Sheep IgE
40	55	56.7	567	6	ABP96588	Abp96588	Pig IgE h
41	53	54.6	341	3	AA06202	Aa06202	Immunogen
42	53	54.6	342	3	AA06201	Aa06201	Immunogen
43	46	47.4	135	2	AAY76530	Aay76530	Human ova
44	46	47.4	135	7	ABO81258	Abo81258	Pseudomon
45	46	47.4	386	8	ADU00341	Adu00341	Iron hydr

ALIGNMENTS

RESULT 1

ADRI0609

ID ADRI0609 standard; peptide; 18 AA.

XX AC ADRI0609;

XX DT 21-OCT-2004 (first entry)

XX DE Dog IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.

XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;

XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX OS Canis familiaris.

XX PN WO2004065936-A2.

XX PD 05-AUG-2004.

XX PF 15-JAN-2004; 2004WO-US003566.

XX PR 16-JAN-2003; 2003US-0440472P.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IgE epitope, useful

XX for testing an allergen reactivity of IgE sample, detecting mammalian IgE

XX or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that

XX specifically binds to a mammalian IgE epitope, where the epitope is

XX between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.

XX (I) is useful for testing an allergen reactivity of an IgE sample. The

XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut

XX and corn allergens. The sample is a biological sample collected from a

XX dog, cat or horse. (I) is also useful for detecting mammalian IgE and for

XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal

XX antibodies recognise epitopes on canine IgE corresponding to amino acid

XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

XX canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.5e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VDGQKATNIPFYTPAGTK 18
 |||||
 DB 1 VDGQKATNIPFYTPAGTK 18

RESULT 2

AAV79995
 ID AAV79995 standard; protein; 312 AA.

XX AAV79995;

XX 15-MAY-2000 (first entry)

XX Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 for immunization against allergy.

XX Example 1; Page 66-68; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IgE, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AAV79994 to AAY80084 represent amino acid
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 312 AA;

Query Match 100.0%; Score 97; DB 3; Length 312;

Best Local Similarity 100.0%; Pred. No. 1.3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTPAGTK 18
 |||||
 DB 48 VDGQKATNIPFYTPAGTK 65

RESULT 3

AAW23067

ID AAW23067 standard; protein; 417 AA.

XX AAW23067;

XX 30-JUN-2005 (revised)

DT 16-JUN-2005 (revised)

DT 19-FEB-1998 (first entry)

XX Canine IgE heavy chain constant region (exon 1-4 product).

XX IgE; immunoglobulin; antibody; heavy chain constant region; allergy;
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

XX Canis familiaris.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX WO9730156-A2.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US002322.

XX 14-FEB-1996; 96US-00601197.

XX (IDEX-) IDEXX LAB INC.

XX Mermer B, Harris RA, Siefring AE;

XX WPI; 1997-425031/39.

DR N-PSDB; AAT79278.

XX Isolated canine IgE heavy chain constant region DNA - useful to develop
 PT products for treatment of canine allergies and for immunomodulation in
 PT dogs.

XX Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to
 CC treat Type I immediate hypersensitivity, and for immunomodulation

CC Revised record issued on 30-JUN-2005 : Typo in comments
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 97; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAGPK 18
 |||||
 Db 141 VDGQKATNIFPYTAGPK 158

RESULT 4

AAR97753
 ID AAR97753 standard; protein; 426 AA.

AC AAR97753;

XX 28-AUG-1996 (first entry)

DE Canine IgE.

XX IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.

XX Canis familiaris.

XX WO9614867-A1.

XX 23-MAY-1996.

XX 03-NOV-1995; 95WO-US013795.

XX 09-NOV-1994; 94US-00336583.

XX 09-NOV-1994; 94US-00336891.

XX (MERI) MERCK & CO INC.

XX Hollis GF, Patel MD;

XX WPI; 1996-277321/28.

XX N-PSDB; AAT29824.

XX New DNA encoding canine IgE and IgA - useful in vaccines, anti-sense
 PT therapy, assays, drug screening, etc.

XX Claim 11; Page 29-30; 49pp; English.

XX The canine IgE amino acid sequence (AAR97753) was deduced from an
 CC isolated gene (AAT29824) obt'd. from a canine liver DNA library. The
 CC cloning of the IgE gene allows prodn. of large quantities of recombinant
 CC IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE
 CC can be used in drug development (e.g. small molecule screening, assay
 CC development and anti-IgE antibody generation). Fragments of IgE can be
 CC used in vaccines or to prevent IgE-mediated hypersensitivity. The new
 CC sequence information permits targeted modulation of IgE-mediated immune
 CC responses

XX Sequence 426 AA;

Query Match 100.0%; Score 97; DB 2; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAGPK 18

Db 146 VDGQKATNIFPYTAGPK 163

RESULT 5

ABP96583

ID ABP96583 standard; protein; 426 AA.

XX
 AC
 XX

ABP96583;

DT 28-MAY-2003 (first entry)

XX Dog IgE heavy chain amino acid sequence SEQ ID NO:28.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;

XX immune response; major histocompatibility complex; MHC; immunogenic;

XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;

XX dermatological; antiinflammatory; IgE-mediated condition; food allergy;

XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;

XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;

XX urticaria hives.

XX Canis familiaris.

OS WO2003015716-A2.

PN 27-FEB-2003.

PD 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

PA Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 CC against IgE, by identifying peptide eliciting CTL response to IgE
 CC peptides naturally presented by major histocompatibility complex class I
 CC protein.

PS Example 7; Page 152-154; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IgE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IgE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IgE peptides, C1-3 have antiallergic, antiasthmatic, immunosuppressive,
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IgE, and in
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IgE heavy chain amino acid
 CC sequence, which is given in an example from the present invention

XX Sequence 426 AA;

Query Match 100.0%; Score 97; DB 6; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAGPK 18

Db 146 VDGQKATNIFPYTAGPK 163

RESULT 6
 ID ADR10610 standard; peptide; 18 AA.
 XX AC ADR10610;
 XX DT 21-OCT-2004 (first entry)
 XX DE
 XX DE Cat IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.
 XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
 XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 XX KW cat.
 XX OS Felis catus.
 XX PN WO2004065936-A2.
 XX PD 05-AUG-2004.
 XX PF 15-JAN-2004; 2004WO-US003566.
 XX PR 16-JAN-2003; 2003US-0440472P.
 XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PI Hammerberg B;
 XX PS WPI; 2004-593545/57.
 XX PT Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.
 XX Example 6; Page 9; 14pp; English.
 CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC cat IgE 3.76 recognition site.
 XX Sequence 18 AA;
 SQ
 Query Match 89.7%; Score 87; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VDGQKATNIFPYTAPG 16
 DB 1 VDGQKATNIFPYTAPG 16
 RESULT 7
 ADG73237
 ID ADG73237 standard; protein; 431 AA.
 XX AC ADG73237;
 XX DT 11-MAR-2004 (first entry)
 XX PF
 XX

DE Cat immunoglobulin E (IgE) constant region.
 XX
 KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
 KW immune response; IgE-mediated response; allergy; cat; constant region.
 XX OS Felis catus.
 XX PN US2003216565-A1.
 XX PD 20-NOV-2003.
 XX PF 07-APR-2003; 2003US-00409772.
 XX PR 07-JAN-1999; 99US-0115033P.
 XX PR 07-JAN-2000; 2000US-00479614.
 XX PA (MCCA/) MCCALL C.
 XX PA (WEBE/) WEBER E.
 XX PI McCall C, Weber E;
 XX WPI; 2004-010802/01.
 XX DR N-PSDB; ADG73236.
 XX PT New isolated nucleic acid molecule encoding a portion of a feline IgE
 PT heavy chain protein, useful for treating and/or eliciting feline immune
 PT responses for IgE-mediated responses, such as allergies.
 XX Claim 12; SEQ ID NO 14; 44pp; English.
 XX CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC portion of a feline IgE heavy chain protein. The methods and compositions
 CC of the present invention are useful for eliciting feline immune responses
 CC for and/or treating IgE-mediated responses, such as allergies. This is
 CC the amino acid sequence of a cat immunoglobulin E (IgE) constant region.
 XX SQ Sequence 431 AA;
 Query Match 89.7%; Score 87; DB 8; Length 431;
 Best Local Similarity 100.0%; Pred. No. 8.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VDGQKATNIFPYTAPG 16
 DB 151 VDGQKATNIFPYTAPG 166
 RESULT 8
 ABP96580
 ID ABP96580 standard; protein; 496 AA.
 XX AC ABP96580;
 XX DT 28-MAY-2003 (first entry)
 XX DE Cat IgE heavy chain amino acid sequence SEQ ID NO:25.
 XX KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KW urticaria hives.
 XX OS Felis catus.
 XX PN WO2003015716-A2.
 XX PD 27-FEB-2003.
 XX PF 08-AUG-2002; 2002WO-US026986.
 XX

PR 13-AUG-2001; 2001US-0312120P.
 XX (IGET-) IGE THERAPEUTICS INC.
 PA Chen SA, Yang Y, Batankiewicz T, Chen Z;
 XX WPI; 2003-268242/26.
 DR
 XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IGE, by identifying peptide eliciting CTL response to IGE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.
 XX
 XX Example 7; Page 145-147; 187pp; English.
 PS
 XX The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IGE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IGE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IGE peptides, C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IGE, and in
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IGE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 XX
 SQ Sequence 496 AA;

Query Match 89.7%; Score 87; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAGP 16
 |||||
 Db 216 VDGQKATNIPFYTAGP 231

RESULT 9
 ABU09338
 ID ABU09338 standard; protein; 496 AA.

XX AC ABU09338;

XX 27-JUN-2003 (first entry)

XX DE Feline IGE epsilon heavy chain #2.

XX KW Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;
 KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;
 KW antibody technology; antiallergic; antiparasitic; cytostatic.

XX OS Felis catus.

XX PN US2003013183-A1.

XX PD 16-JAN-2003.

XX PF 07-JAN-2000; 2000US-00479614.

XX PR

PR 07-JAN-1999; 99US-0115033P.
 XX (MCCA/) MCCALL C.
 PA (WEBE/) WEBER E.
 XX
 XX McCall C, Weber E;
 XX WPI; 2003-391997/37.
 DR N-PSDB; ABX95715.
 XX
 PT New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or
 PT light chain protein, useful for treating feline IGE-mediated responses
 PT e.g. allergies, parasitic infections or neoplasia.
 XX
 PS Claim 1; Page 37-39; 45pp; English.
 XX
 CC The present invention relates to the isolation of feline immunoglobulin E
 CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the
 CC polynucleotide sequences encoding them. The sequences of the invention
 CC are useful for treating feline IGE-mediated immune responses (e.g.
 CC allergies, parasitic infections or neoplasia), in vaccine technology,
 CC small molecule/antibody technology, molecular biology, and various
 CC immunological techniques related to feline IGE and its functions. The
 CC present sequence represents feline IGE epsilon heavy chain #2
 XX
 SQ Sequence 496 AA;
 Query Match 89.7%; Score 87; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VDGQKATNIPFYTAGP 16
 |||||
 Db 216 VDGQKATNIPFYTAGP 231

RESULT 10
 ABU09336
 ID ABU09336 standard; protein; 496 AA.
 XX AC ABU09336;
 XX
 XX 27-JUN-2003 (first entry)
 XX DE Feline IGE epsilon heavy chain #1.
 XX KW Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;
 KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;
 KW antibody technology; antiallergic; antiparasitic; cytostatic.
 XX OS Felis catus.
 XX
 XX PH Location/Qualifiers
 XX FT 66..496
 XX FT /note= "This sequence is given as SEQ ID No:14 and is
 specifically claimed in Claim 12"
 XX FT 284..309
 XX FT /note= "This sequence is given as SEQ ID No:11 and is
 specifically claimed in Claim 9"
 XX FT 288..305
 XX FT /note= "This sequence is given as SEQ ID No:8 and is
 specifically claimed in Claim 10"
 XX FT 291..302
 XX FT /note= "This sequence is given as SEQ ID No:5 and is
 specifically claimed in Claim 11"
 XX
 XX PN US2003013183-A1.
 XX PD 16-JAN-2003.
 XX PF 07-JAN-2000; 2000US-00479614.
 XX PR 07-JAN-1999; 99US-0115033P.


```

RESULT 13
ID ABP96584 standard; protein; 577 AA.
XX AC ABP96584;
XX DT 28-MAY-2003 (first entry)
XX DE Duckbilled platypus IgE heavy chain amino acid sequence SEQ ID NO:29.
XX KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
XX KW immune response; major histocompatibility complex; MHC; immunogenic;
XX KW anti-allergic; antiallergic; immunosuppressive; vasotropic; cytostatic;
XX KW dermatological; anti-inflammatory; IgE-mediated condition; food allergy;
XX KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX KW urticaria hives.
XX OS Ornithorhynchus anatinus.
XX PN WO2003015716-A2.
XX PN WO2003015716-A2.
XX PD 27-FEB-2003.
XX PF 08-AUG-2002; 2002WO-US026986.
XX PR 13-AUG-2001; 2001US-0312120P.
XX PA (IGET-) IGE THERAPEUTICS INC.
XX PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX DR WPI; 2003-268242/26.
XX PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
XX PT against IgE, by identifying peptide eliciting CTL response to IgE
XX PT peptides naturally presented by major histocompatibility complex class I
XX PS protein.
XX PS Example 7; Page 154-157; 187pp; English.
XX CC The present invention describes a method (M1) for identifying peptides
XX CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
XX CC E (IgE), comprising providing a test peptide (T) suspected of being able
XX CC to bind to major histocompatibility complex (MHC) class I molecule, and
XX CC evaluating (T) for ability to elicit in a mammal a CTL response to
XX CC naturally processed and presented IgE peptides, where a peptide that
XX CC induces such a response is identified. Also described are compositions:
XX CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
XX CC (C2) comprising at least one isolated polynucleotide encoding (I); and
XX CC (C3) comprising antigen-presenting cells that recognise at least one (I).
XX CC Where C1-3 are able to bind to at least one MHC class I molecule and to
XX CC elicit in a mammal a CTL response to naturally processed and presented
XX CC IgE peptides. C1-3 have anti-allergic, antiallergic, immunosuppressive,
XX CC vasotropic, dermatological, anti-inflammatory and cytostatic activities,
XX CC and can be used as inducers of a CTL response against IgE, and in
XX CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
XX CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
XX CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
XX CC useful for treating atopic hypersensitivity conditions (such as allergic
XX CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
XX CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
XX CC hives). The present sequence represents an IgE heavy chain amino acid
XX CC sequence, which is given in an example from the present invention
XX SQ
XX Sequence 577 AA;
Query Match 75.3%; Score 73; DB 6; Length 577;
Best Local Similarity 86.7%; Pred. No. 0.0026;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 14
ID AAB06204 standard; protein; 343 AA.
XX AC AAB06204;
XX DT 22-NOV-2000 (first entry)
XX DE Platypus IgE heavy chain constant regions 2, 3 and 4.
XX KW Platypus; immunoglobulin E; IgE; vaccination; infection; allergy; asthma;
XX KW eczema; immunogenic peptide.
XX OS Ornithorhynchus anatinus.
XX PN WO2000025722-A2.
XX PN 11-MAY-2000.
XX PF 21-OCT-1999; 99WO-SE001896.
XX PR 02-NOV-1998; 98US-0106652P.
XX PR 22-SEP-1999; 99US-00401636.
XX PA (RESI-) RESISTENTIA PHARM AB.
XX PI Hellman LT;
XX DR WPI; 2000-365342/31.
XX PT Immunogenic polypeptides useful for preventing the harmful effects of
XX PT immunoglobulin E in mammals.
XX PS Disclosure; Fig 2; 50pp; English.
XX CC The present sequence is an immunogenic peptide consisting of the heavy
XX CC chain constant regions 2, 3 and 4 of the platypus IgE. It was used to
XX CC construct a number of immunogenic peptides which consisted of regions of
XX CC IgE from different mammals, which appear to cause a stronger polyclonal
XX CC anti-self IgE response than peptides consisting of the same regions from
XX CC one mammal. Immunogenic peptides, particularly those consisting of
XX CC different heavy chain constant regions, can be used for vaccination in
XX CC humans, against bacterial and viral infections and allergies, such as
XX CC asthma, fur, pollen and food allergies and eczema
XX SQ
XX Sequence 343 AA;
Query Match 70.1%; Score 68; DB 3; Length 343;
Best Local Similarity 80.0%; Pred. No. 0.01;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
ID ADF90022 standard; protein; 337 AA.
XX AC ADF90022;
XX DT 26-FEB-2004 (first entry)

```

```

XX Opossum-rat chimeric IgE polypeptide.
XX DE
XX KW IGE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;
XX KW antiasthmatic; dermatological.
XX OS
XX OS Chimeric.
XX OS Didelphis virginiana.
XX OS Rattus sp.
XX PN WO2003096966-A2.
XX XX
XX PD 27-NOV-2003.
XX XX
XX PF 15-MAY-2003; 2003WO-IB002503.
XX XX
XX PR 21-MAY-2002; 2002US-0382552P.
XX XX
XX PA (RESI-) RESISTENTIA PHARM AB.
XX XX
XX PI Lundgren M, Fuentes A, Magnusson A;
XX XX
XX DR WPI; 2004-042496/04.
XX DR N-PSDB; ADF90020, ADF90021.
XX XX
XX PT New host cell comprising a nucleic acid vector comprising a
XX PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or
XX PT SV40 late polyadenylation sequence, useful in producing a chimeric IGE
XX PT polypeptide.
XX XX
XX PS Claim 3; SEQ ID NO 3; 23pp; English.
XX XX
XX CC The present sequence is the protein sequence of an opossum CH2-rat CH3-
XX CC opossum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic
XX CC acid encoding ORO can be used for recombinant production of this chimeric
XX CC IGE in host, e.g. CHO, cells. The invention provides methods and
XX CC materials related to expressing chimeric IgE proteins. Nucleic acid
XX CC vectors, host cells, and methods for producing chimeric IgE polypeptides
XX CC are provided. When administered to a mammal, the chimeric polypeptides
XX CC can reduce the IgE antibody effects of IgE-related diseases such as
XX CC asthma, allergies and eczema.
XX XX
XX SQ Sequence 337 AA;

Query Match 59.8%; Score 58; DB 8; Length 337;
Best Local Similarity 76.9%; Pred. No. 0.48;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYT 13
DB |||||:|:||||
56 VDGQEAENLFPYT 68

Search completed: August 30, 2006, 04:22:02
Job time : 65.4545 secs

```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 10.7273 Seconds
(without alignments)
161.448 Million cell updates/sec

Title: US-10-758-165a-9
Perfect score: 97
Sequence: 1 VDGQKATNIFPYTAPG 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.5	270	2	T16880
2	46	47.4	579	2	JW0071
3	46	47.4	586	2	asparagine synthas
4	46	47.4	658	2	asparagine synthas
5	45	46.4	350	2	probable surface p
6	45	46.4	350	2	sensor histidine k
7	45	46.4	350	2	histidine kinase (
8	44	45.4	583	1	asparagine synthas
9	43	44.3	511	2	hypothetical prote
10	43	44.3	322	2	transporter BME18
11	42	43.3	258	2	asparagine synthas
12	42	43.3	381	2	putative trans-acon
13	42	43.3	476	2	ATP-binding protei
14	42	43.3	623	2	6-phosphogluconate
15	42	43.3	683	2	hypothetical prote
16	42	43.3	1686	2	conserved hypothet
17	41	42.3	241	2	conserved hypothet
18	41	42.3	272	2	hypothetical prote
19	41	42.3	359	2	probable conserved
20	41	42.3	570	2	vacuolar protein s
21	41	42.3	619	2	hypothetical prote
22	41	42.3	643	1	El protein - human
23	41	42.3	713	2	NADPH-cytochrome P
24	41	42.3	859	2	hypothetical prote
25	41	42.3	909	2	aspartate kinase (
26	41	42.3	916	2	aspartate kinase (
27	41	42.3	1032	2	hypothetical prote
28	41	42.3	1055	2	multidrug-efflux c
29	40.5	41.8	795	2	hypothetical prote

30	40	41.2	101	2	G69203
31	40	41.2	109	2	F89886
32	40	41.2	137	2	A83751
33	40	41.2	179	2	D90167
34	40	41.2	189	2	S49846
35	40	41.2	217	1	GMBPT4
36	40	41.2	227	2	C75582
37	40	41.2	240	2	C89967
38	40	41.2	302	2	T03109
39	40	41.2	327	2	S40753
40	40	41.2	357	1	A48511
41	40	41.2	374	2	G81926
42	40	41.2	419	2	C81179
43	40	41.2	454	2	AH2821
44	40	41.2	470	2	H97599
45	40	41.2	584	2	T12989

ALIGNMENTS

RESULT 1

T16880
hypothetical protein T14G12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-Oct-2004
C;Accession: T16880
R;Wilcox, L.

submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid T14G12.
A;Reference number: Z18596
A;Accession: T16880
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-270 <WT>
A;Cross-references: UNIPROT:Q22510; UNIPARC:UPI0000075025; EMBL:U41268; NID:g1086843; PIDN:PI1086843; PIDN:PI1086843
A;Gene: CESP:T14G12.4
A;Introns: 37/1; 72/3; 164/1
F;93-185/Domain: fork head DNA-binding domain homology <FHD>

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIFPYTAPG 16

Db 205 GAAANLFPYFSPG 218

RESULT 2

JW0071
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - soybean
C;Species: Glycine max (soybean)
C;Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Accession: JW0071
R;Yamagata, H.; Nakajima, A.; Bowler, C.; Iwasaki, T.
Biosci. Biotechnol. Biochem. 62, 148-150, 1998
A;Title: Molecular cloning and characterization of a cDNA encoding asparagine synthetase
A;Reference number: JW0071; MUID:98162148; PMID:9501527
A;Accession: JW0071
A;Molecule type: mRNA
A;Residues: 1-579 <YAM>

A;Cross-references: UNIPROT:Q42792; UNIPARC:UPI00000A95EC; GB:U55874; NID:g1305548; PIDN:PIDN
C;Superfamily: asparagine synthase (glutamine-hydrolysing)
C;Keywords: asparagine biosynthesis; ligase
F;2-579/Product: asparagine synthase (glutamine-hydrolysing) #status predicted <DUM>
F;2/Active site: Cys #status predicted

Query Match 47.4%; Score 46; DB 2; Length 579;
Best Local Similarity 34.4%; Pred. No. 10;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

```

Qy 1 VDQK-----ATNIPPYTAGTK 18
      |||  |||  |||  |||  |||  |||
Db 462 IDGLKAHAEKHVTRDMLNANIPFNTPTTK 493

RESULT 3
S69183
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - Lotus japonicus
C;Species: Lotus japonicus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69183; S57932
R;Waterhouse, R.N.; Smyth, A.J.; Massonneau, A.; Prosser, I.M.; Clarkson, D.T.
Plant Mol. Biol. 30, 883-897, 1996
A;Title: Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus
A;Reference number: S69182; MUID:96270368; PMID:8639748
A;Accession: S69183
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-586 <WAT>
A;Cross-references: UNIPROT:P49093; UNIPARC:UPI000016DE2B; EMBL:X89410; NID:g897772; PID:
A;Experimental source: strain B-129
C;Genetics:
A;Gene: AS2
C;Superfamily: asparagine synthase (glutamine-hydrolyzing)
C;Keywords: asparagine biosynthesis; ligase
F;2-586/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <DUM>
F;2/Active site: Cys #status predicted

      Query Match 47.4%; Score 46; DB 2; Length 586;
      Best Local Similarity 31.2%; Pred. No. 10;
      Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;

Qy 1 VDQK-----ATNIPPYTAGTK 18
      |||  |||  |||  |||  |||  |||
Db 462 IDGLKDHAAKHVTDKMLNAGNIYFNTPTTK 493

RESULT 4
AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0110
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0110
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-658 <KUR>
A;Cross-references: UNIPROT:Q8ZHU0; UNIPARC:UPI00000CD765; GB:AL590842; PIDN:CAC89747.1;
C;Genetics:
A;Gene: YPO0902

      Query Match 47.4%; Score 46; DB 2; Length 658;
      Best Local Similarity 52.9%; Pred. No. 12;
      Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQKATNIPFYTAGT 17
      ::|||::|
Db 99 LMGKATNLAPATISST 115

RESULT 5
G95009
sensor histidine kinase [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95009
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

```

```

on, J.D.; Umavam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, J.
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95009
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <KUR>
A;Cross-references: UNIPROT:Q9S1J1; UNIPARC:UPI0000051BF0; GB:AE005672;
C;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0084

      Query Match 46.4%; Score 45; DB 2; Length 350;
      Best Local Similarity 72.7%; Pred. No. 8.6;
      Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 NIPPYTAGTK 18
      |||  |||  |||  |||  |||  |||
Db 248 NAFKYSAPGTK 258

RESULT 6
E97881
histidine kinase (EC 2.7.3.-) [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: E97881
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: E97881
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <KUR>
A;Cross-references: UNIPROT:Q9S1J1; UNIPARC:UPI0000051BF0; GB:AE007317;
C;Genetics:
A;Gene: hk08
C;Keywords: phosphotransferase

      Query Match 46.4%; Score 45; DB 2; Length 350;
      Best Local Similarity 72.7%; Pred. No. 8.6;
      Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 NIPPYTAGTK 18
      |||  |||  |||  |||  |||  |||
Db 248 NAFKYSAPGTK 258

RESULT 7
AJPMN2
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) [similarity] - garden pea
N;Alternate names: asparagine synthetase (glutamine-hydrolyzing)
C;Species: Pisum sativum (garden pea)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: S11443
R;Tsai, F.Y.; Coruzzi, G.M.
EMBO J. 9, 323-332, 1990
A;Title: Dark-induced and organ-specific expression of two asparagine synthetase genes i
A;Reference number: S11443; MUID:90151604; PMID:1968003
A;Accession: S11443
A;Molecule type: DNA
A;Residues: 1-583 <TSA>
A;Cross-references: UNIPROT:P19252; UNIPARC:UPI000016DF0B; EMBL:X52180; NID:g20651; PIDN:
C;Genetics:
A;Gene: AS2
C;Superfamily: asparagine synthase (glutamine-hydrolyzing)

```

AJPWN1
 asparagine synthase [glutamine-hydrolysing] (EC 6.3.5.4) [similarity] - garden pea
 N;Alternate names: asparagine synthetase (glutamine-hydrolyzing)
 C;Species: Pisum sativum (garden pea)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: S11444
 R;Tsai, F.Y.; Coruzzi, G.M.
 EMBO J. 9, 323-332, 1990
 A;Title: Dark-induced and organ-specific expression of two asparagine synthetase genes 1
 A;Reference number: S11443; MUID:90151604; PMID:1968003
 A;Accession: S11444
 A;Molecule type: DNA
 A;Residues: 1-586 <TSA>
 A;Cross-references: UNIPROT:P19251; UNIPARC:UPI000016DFOA; EMBL:XS2179; NID:G20649; PIDN
 C;Comment: This protein is one of a family of glutamine amidotransferases that have dual
 : an aminator domain, which catalyzes the ammonia-dependent reaction, and a glutamine am
 C;Genetics:
 A;Gene: ASI
 C;Superfamily: asparagine synthase (glutamine-hydrolyzing)
 C;Keywords: asparagine biosynthesis; ligase
 F;2-586/Product: asparagine synthase [glutamine-hydrolyzing] #status predicted <MAT>
 F;175-586/Domain: aminator <AMN>
 F;2/Active site: Cys #status predicted

Query Match	44.3%;	Score 43;	DB 1;	Length 586;
Best Local Similarity	53.8%;	Pred. No. 33;	Mismatches 3;	Indels 0;
Matches	7;	Conservative 3;	Gaps 0;	

QY 6 ATNIFPYTAPGTK 18

DB 482 ASHIFPNTPTNK 494

```

      |||:|:|:|:|:|
      |||:|:|:|:|:|
  
```

RESULT 11
 AF0306
 putative trans-aconitate methyltransferase (EC 2.1.1.-) [imported] - Yersinia pestis (str
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AF0306
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 denc-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AF0306
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-258 <KUR>
 A;Cross-references: UNIPROT:Q8ZDP7; UNIPARC:UPI00001368D0; GB:AL590842; PIDN:CAC91314.1;
 C;Genetics:
 A;Gene: tam
 C;Superfamily: bioC protein; bioC homology
 C;Keywords: methyltransferase

Query Match	43.3%;	Score 42;	DB 2;	Length 258;
Best Local Similarity	50.0%;	Pred. No. 20;	Mismatches 6;	Indels 0;
Matches	9;	Conservative 3;	Gaps 0;	

QY 1 VDGKATNIFPYTAPGTK 18

DB 200 VDWLRGTLRPYLPLTE 217

```

      |||:|:|:|:|:|
      |||:|:|:|:|:|
  
```

RESULT 12
 AD2436
 ATP-binding protein of polyamine ABC transporter all5044 [imported] - Nostoc sp. (strain
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004
 C;Accession: AD2436
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; UID:21595285; PMID:11759840
A;Accession: AD2436
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <KUR>
A;Cross-references: UNIPROT:Q8YMW92; UNIPARC:UPI00000CED3F; GB:BA0000019; PIDN:BA076743.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all15044

Query Match 43.3%; Score 42; DB 2; Length 381;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAP 15
Db 80 IQGQPMWINIPYRPP 94
|||||
|

RESULT 13
AC2465
6-phosphogluconate dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC2465
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; UID:21595285; PMID:11759840
A;Accession: AC2465
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <KUR>
A;Cross-references: UNIPROT:Q8YLM3; UNIPARC:UPI000000CE80D; GB:BA0000019; PIDN:BA076974.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr5275
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate dehydrogenase

Query Match 43.3%; Score 42; DB 2; Length 476;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 NIPFYTAPGK 18
Db 238 NIPFYDPETK 248
|||||
|

RESULT 14
T22177
hypochemical protein F44Fl.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22177
R;Dobson, R.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19527
A;Accession: T22177
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-623 <WIL>
A;Cross-references: UNIPROT:O02260; UNIPARC:UPI000017B9C4; EMBL:Z81083; PIDN:CAB03101.1;
A;Experimental source: clone F44F1
C;Genetics:
A;Gene: CESP:F44Fl.3
A;Map position: 1
A;Introns: 43/2; 69/3; 181/3; 241/2; 493/3; 526/2; 548/3

Query Match 43.3%; Score 42; DB 2; Length 623;

Best Local Similarity 50.0%; Pred. No. 53;
Matches 11; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

Qy 1 VDGQKATNI-----FPYTAPGK 18
Db 152 VDGQWKTIIDDDYFPYTTDGIR 173
|||||
|

RESULT 15

B71325

conserved hypothetical protein TP0421 - syphilis spirochete

C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C;Accession: B71325

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin-

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo-

rney, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; UID:98332770; PMID:9665876

A;Accession: B71325

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-683 <COL>

A;Cross-references: UNIPROT:O83436; UNIPARC:UPI000000COA71; GB:AE001220; GB:AE000520; NID

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0421

Query Match 43.3%; Score 42; DB 2; Length 683;

Best Local Similarity 50.0%; Pred. No. 59;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIPFYTAPG 16

Db 278 GQKSARFFGFSAPG 291
|||||
|

Search completed: August 30, 2006, 04:30:53

Job time : 12.7273 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:22:32 ; Search time 70.1818 Seconds
(without alignments)
237.245 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDGQKATNIFPYTAPGK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	54.6	1143	2	Q3N7V1_9PROT
2	51	52.6	382	2	Q7P5V1_FUSNV
3	51	52.6	382	2	Q8R6B3_FUSNN
4	48	49.5	168	2	Q95Q49_CAEEL
5	48	49.5	270	2	Q22510_CAEEL
6	47	48.5	365	2	Q36VP1_RHOA
7	47	48.5	1054	2	Q608X6_METCA
8	47	48.5	1538	2	Q94H26_ORYSA
9	46	47.4	497	2	Q9FYU1_CHLRE
10	46	47.4	579	2	P93168_SOYEN
11	46	47.4	579	2	Q38TA6_SOYEN
12	46	47.4	579	2	Q42792_SOYEN
13	46	47.4	579	2	Q9SM55_PHAVU
14	46	47.4	585	1	ASNS2_LOTJA
15	46	47.4	641	2	Q8CKM1_YERPE
16	46	47.4	658	2	Q8ZHJ0_YERPE
17	45.5	46.9	491	2	Q212W7_BORAV
18	45	46.4	185	2	Q2T7B0_ASPOV
19	45	46.4	190	2	Q68E47_AERPU
20	45	46.4	279	2	Q619H6_CAEER
21	45	46.4	350	2	Q8DRK0_STRR6
22	45	46.4	350	2	Q9SLJ1_STRPN
23	45	46.4	445	1	ALN_STRCO
24	45	46.4	582	1	ASNS2_PEA
25	45	46.4	583	2	Q8RVL0_9FABA
26	44	45.4	131	1	SSB_STAES
27	44	45.4	131	2	Q5HMC5_STAEO
28	44	45.4	190	2	Q3VAY9_SPHPN
29	44	45.4	340	2	Q9AYA0_ORYSA
30	44	45.4	395	2	Q9ZHQ4_STRFR
31	44	45.4	476	2	Q3MA44_ANAVT

32	44	45.4	511	1	U171_CAEEL
33	44	45.4	525	2	Q6ALL1_DESPS
34	44	45.4	584	2	Q9MB61_ASTSI
35	44	45.4	586	2	Q84X69_9FABA
36	44	45.4	589	2	Q53004_ORYSA
37	44	45.4	703	2	Q46LV7_PROWT
38	44	45.4	760	2	Q6UUM4_ORYSA
39	44	45.4	875	2	Q7FAL9_ORYSA
40	44	45.4	884	2	Q53JX1_ORYSA
41	44	45.4	908	2	Q2ZH01_CALSA
42	44	45.4	1436	2	Q7FAL2_ORYSA
43	44	45.4	1685	2	Q7XSP1_ORYSA
44	44	45.4	1829	2	Q70XV6_AMBTC
45	44	45.4	2096	2	Q2R0G5_ORYSA

ALIGNMENTS

RESULT 1
Q3N7V1_9PROT
ID Q3N7V1_9PROT PRELIMINARY; PRT; 1143 AA.
AC Q3N7V1;
DT 25-OCT-2005, integrated into UniprotKB/TREMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Putative type 4 fibrillar biogenesis protein PilY precursor.
GN ORFNames=NeutDRAFT_0559;
OS Nitrosomonas eutropha C71.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=335283;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C71;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Nitrosomonas eutropha C71."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C71;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M., Hauser L.;
RT "Annotation of the draft genome assembly of Nitrosomonas eutropha C71."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -|- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AJAEJ01000019; EAC16686.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 1143 AA; 123766 MW; 9C270A88F6A0FAF1 CRC64;
Potential.
Query Match 54.6%; Score 53; DB 2; Length 1143;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 2 DGQKATNIFPYTAPGT 17
||| ||||| :|||
Db 383 DGSKLTHNFFNTSPAT 398
RESULT 2
Q7P5V1_FUSNV
ID Q7P5V1_FUSNV PRELIMINARY; PRT; 382 AA.

```

AC Q7P5VL;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (BC 4.2.1.1.-).
GN Name=PNV1343;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 49256;
RA Kapatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyrpides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAF01000055; EAA24105.1; -; Genomic_DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR010327; HGD-D.
DR Pfam; PF06050; HGD-D; 1.
DR Lyase.
SQ SEQUENCE 382 AA; 43893 MW; 441C73816E1C761E CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGOKATNIFPYTPAP 15
Db 28 EGKXAVGIFPYAP 41

RESULT 3
Q8R6B3_FUSNN PRELIMINARY; PRT; 382 AA.
AC Q8R6B3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.1.-).
GN OrderedLocustNames=FN0208;
OS Fusobacterium nucleatum subsp. nucleatum.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=1189109;
RA DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fongstein M., Kyrpides N.C., Overbeek R.;
RL "Genome sequence and analysis of the oral bacterium Fusobacterium
RL nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE009951; AAL94414.1; -; Genomic_DNA.
DR BiOCYC; FNUC190304:FN0208-MONOMER; -.
DR GO; GO:0016829; F:lyase activity; IEA.

DR InterPro; IPR010327; HGD-D.
DR Pfam; PF06050; HGD-D; 1.
DR Complete proteome; Lyase.
SQ SEQUENCE 382 AA; 43923 MW; 93038D4296AE34CD CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGOKATNIFPYTPAP 15
Db 28 EGKXAVGIFPYAP 41

RESULT 4
Q95QA9_CAEEL PRELIMINARY; PRT; 168 AA.
AC Q95QA9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Forkhead transcription factor family protein 2, isoform b.
GN Name=fkh-2; ORFNames=TL4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; U41268; AAL02521.1; -; Genomic_DNA.
DR HSP; Q99958; IDSV.
DR SMR; Q95QA9; 2-68.
DR Ensembl; TL4G12.4; Caenorhabditis elegans.
DR WormBase; WSGene00001434; fkh-2.
DR WormPepe; TL4G12.4b; CR29342.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 168 AA; 19239 MW; 8E01AC4EG9968572 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQKATNIFPYTPAG 16
Db 103 GAARANLFPYFSPG 116

RESULT 5
Q22510_CAEEL PRELIMINARY; PRT; 270 AA.
ID Q22510_CAEEL

```

AC Q22510;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 39.
 DE Forkhead transcription factor family protein 2, isoform a.
 GN Name=Fkh-2; ORFNames=TI4G12.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 CC -1- INTERACTION:
 CC Q2XW88:phd-3; NbExp=1; IntAct=EBI-327741, EBI-316766;
 CC T16848:RO2F2.5; NbExp=1; IntAct=EBI-327741, EBI-314179;
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; U41268; AAA82436.1; -; Genomic_DNA.
 DR PIR; T16880; T16880.
 DR HSP; Q99958; I05V.
 DR SMR; Q22510; 93-170.
 DR IntAct; Q22510; -.
 DR Ensembl; T14G12.4; Caenorhabditis elegans.
 DR WormBase; WBGene00001434; fkh-2.
 DR WormPep; T14G12.4a; CE04965.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR001766; TF Fork head.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 DR Pfam; PF00250; Fork head; 1.
 DR PRINTS; PR00053; FORKHED.
 DR ProDom; PD000425; TF Fork head; 1.
 DR SMART; SM00339; FH; 1.
 DR PROSITE; PS00657; FORK HEAD 1; 1.
 DR PROSITE; PS00658; FORK HEAD 2; 1.
 DR PROSITE; PS00039; FORK HEAD 3; 1.
 KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
 KW Transcription regulation.
 SQ SEQUENCE 270 AA; 30491 MW; 7C49116B5EC76175 CRC64;
 Query Match 49.5%; Score 48; DB 2; Length 270;
 Best Local Similarity 57.1%; Pred. No. 24;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GQKATNIFPYTAPG 16
 DB 205 GAAANLFPYFSPG 218
 RESULT 6
 ID Q36VF1_RHOPA
 AC Q36VF1; PRELIMINARY; PRT; 365 AA.
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=RPEDRAFT_0215;
 OS Rhodopseudomonas palustris BisA53.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=316055;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BisA53;
 Query Match 49.5%; Score 48; DB 2; Length 270;
 Best Local Similarity 57.1%; Pred. No. 24;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GQKATNIFPYTAPG 16
 DB 205 GAAANLFPYFSPG 218
 RESULT 6
 ID Q36VF1_RHOPA
 AC Q36VF1; PRELIMINARY; PRT; 365 AA.
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=RPEDRAFT_0215;
 OS Rhodopseudomonas palustris BisA53.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=316055;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BisA53;

RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hamon N., Israni S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of Rhodopseudomonas
 RT palustris BisA53."
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BisA53;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome of Rhodopseudomonas palustris
 RT BisA53."
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; AALA0100029; EAO87857.1; -; Genomic_DNA.
 DR KW Hypothetical protein.
 SQ SEQUENCE 365 AA; 40239 MW; E11D3C9BC0F1244F CRC64;
 Query Match 48.5%; Score 47; DB 2; Length 365;
 Best Local Similarity 50.0%; Pred. No. 48;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 VDGQKATNIFPYTAPG 16
 DB 75 LDGLKAGQVIFLPG 90
 RESULT 7
 ID Q608X6_METCA
 AC Q608X6; PRELIMINARY; PRT; 1054 AA.
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE Hydrophobe/amphiphile Efflux-1 (HAEL) family protein.
 GN OrderedLocNames=MCA1360;
 OS Methylococcus capsulatus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
 OC Methylococcaceae; Methylococcus.
 OX NCBI_TaxID=414;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bath / NCIMB 11132;
 RX PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
 RA Ward N.L., Larsen O., Sakwa J., Bruseh L., Khouri H.M., Durkin A.S.,
 RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
 RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,
 RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,
 RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
 RA Grindhaug S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S.,
 RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,
 RA Eisen J.A.;
 RT "Genomic insights into methanotrophy: the complete genome sequence of
 RT Methylococcus capsulatus (Bath).";
 RL PLoS Biol. 2:1616-1628(2004).
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC EMBL; AE017282; AAU92574.1; -; Genomic_DNA.
 DR TIGR; MCA1360; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001036; Acrflvln_res.
 DR InterPro; IPR004764; HAE1.

```

DR Pfam: PF00873; ACR tran: 1.
DR PRINTS: PR00702; ACRIFLAVINRP.
DR TIGRFAMs: TIGR00915; 2A0602; 1.
KW Complete proteome.
SQ SEQUENCE 1054 AA; 115005 MW; BB032CB91B38D1A8 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1054;
Best Local Similarity 56.2%; Pred. No. 1.5e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGP 16
   |:|:|:|:|:|:|:|:|:|
Db 294 VNGHKSTQIVVYTLPG 309

RESULT 8
Q94H26 Oryza
ID Q94H26 Oryza PRELIMINARY; PRT; 1538 AA.
AC Q94H26
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 18.
DE Putative gag-pol polyprotein.
GN Name=OSJNBa0077G22.13;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Frazer C.M.;
RA "Oryza sativa chromosome 3 BAC OSJNBa0077G22 genomic sequence.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AC084831; AAK52152.1; -; Genomic_DNA.
DR Gramene; Q94H26; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0015074; P:DNA integration; IEA.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR008916; Retrov capsid_C.
DR InterPro; IPR002156; RNase_H.
DR InterPro; IPR001584; Rve.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR PROSITE; PS00994; INTEGRASE; 1.
DR PROSITE; PS00879; RNASE_H; 1.
KW Polyprotein.
SQ SEQUENCE 1538 AA; 174629 MW; 5E7A521B398BC776 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1538;
Best Local Similarity 61.5%; Pred. No. 2.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGP 13
   |:|:|:|:|:|:|:|:|:|
Db 740 VDGRAAVNLMPYT 752

RESULT 9

```

```

Q9FYU1 ChLRE
ID Q9FYU1 ChLRE PRELIMINARY; PRT; 497 AA.
AC Q9FYU1
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Fe-hydrogenase precursor (EC 1.18.99.1) (Iron-hydrogenase HydA1).
GN Name=hyd1; Synonyms=hydA, hydA1;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C9;
RA Mets L.J.;
RA "The iron hydrogenase of Chlamydomonas reinhardtii has a single
RT folding domain containing an H-cluster catalytic center and lacking
RT bound electron carriers.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=21gr;
RA Forestier M., Zhang L., Plummer S., Ahmann D., Seibert M.,
RA Ghirardi M.L.;
RA "Two putative Fe-only hydrogenases cloned from Chlamydomonas
RT reinhardtii are coexpressed in cells undergoing anaerobiosis.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Kaminski A.U., Happe T.;
RA "Isolation and characterization of the hydA gene encoding the Fe-
RT hydrogenase of Chlamydomonas reinhardtii.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Happe T., Kaminski A.;
RA "Isolation and characterization of the hydA gene encoding the Fe-
RT hydrogenase of Chlamydomonas reinhardtii.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF289201; AAC00591.1; -; mRNA.
DR EMBL; AY055755; AAL23572.1; -; mRNA.
DR EMBL; AJ012098; CAC80065.1; -; mRNA.
DR EMBL; AJ308413; CAC83731.1; -; Genomic_DNA.
DR HSSP; P07598; 1HFE.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0008901; F:ferredoxin hydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR004108; Fe_hyd_1g_C.
DR InterPro; IPR003149; Fe_hyd_SSU.
DR Pfam; PF02906; Fe_hyd_1g_C; 1.
DR Pfam; PF02256; Fe_hyd_SSU; 1.
DR Oxidoreductase; Signal; Transmembrane peptide.
KW TRANSIT 1 56 Potential.
FT CHAIN 57 497 Fe-hydrogenase.
SQ SEQUENCE 497 AA; 53112 MW; 2E618A259E6572F4 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 497;
Best Local Similarity 55.6%; Pred. No. 99;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGP 18
   |:|:|:|:|:|:|:|:|:|
Db 324 MDGIKETNITMVPAGSK 341

RESULT 10
P93168_SOYBN

```

P93168 SOYBN PRELIMINARY; PRT; 579 AA.
AC P93168;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Asparagine synthetase 1 (EC 6.3.5.4).
GN Name:AS1;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Century;
RX MEDLINE=97188563; PubMed=9037148; DOI=10.1023/A:1005784202450;
RA Hughes C.A., Beard H.S., Matthews B.F.;
RT "Molecular cloning and expression of two cDNAs encoding asparagine
RT synthetase in soybean.";
RL Plant Mol. Biol. 33:301-311(1997).
CC
CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; U77679; AAC49614.1; -; mRNA.
DR HSSP; P22106; ICT9.
DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006426; Asn_synth_AEB.
DR InterPro; IPR001962; Asn_synthase.
DR InterPro; IPR00583; GATase_2.
DR Pfam; PF00733; Asn_synthase; 1.
DR Pfam; PF00310; GATase_2; 1.
DR TIGRFAMs; TIGR01536; asn_synth_AEB; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
KW Ligase.
SQ SEQUENCE 579 AA; 65366 MW; F7E80DA2019B0FC5 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 579;
Best Local Similarity 34.4%; Pred. No. 1.2e+02;
Matches 1; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

QY 1 VDQGK-----ATNIPPYTPAGTK 18
DB 462 IDGLKAHAEKHVTDRLMLNANIFFPNTPTTK 493

RESULT 11
Q381A6 SOYBN PRELIMINARY; PRT; 579 AA.
AC Q381A6;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Asparagine synthetase.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin S., Xiang W., Fan Z.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; DQ227307; ABB04097.1; -; mRNA.

DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
SQ SEQUENCE 579 AA; 65219 MW; 3F3A9F62EA447A17 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 579;
Best Local Similarity 34.4%; Pred. No. 1.2e+02;
Matches 1; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

QY 1 VDQGK-----ATNIPPYTPAGTK 18
DB 462 IDGLKAHAEKHVTDRLMLNANIFFPNTPTTK 493

RESULT 12
Q42792 SOYBN PRELIMINARY; PRT; 579 AA.
AC Q42792;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Asparagine synthetase (EC 6.3.5.4).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Corsoy;
RX MEDLINE=98162148; PubMed=95015127;
RA Yamagata H., Nakajima A., Bowler C., Iwasaki T.;
RT "Molecular cloning and characterization of a cDNA encoding asparagine
RT synthetase from soybean (Glycine max L.) cell cultures.";
RL Biosci. Biotechnol. Biochem. 62:148-150(1998).
CC
CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; U55874; AAC09952.1; -; mRNA.
DR PIR; JMW0071; JMW0071.
DR HSSP; P22108; ICT9.
DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006426; Asn_synth_AEB.
DR InterPro; IPR001962; Asn_synthase.
DR InterPro; IPR00583; GATase_2.
DR Pfam; PF00733; Asn_synthase; 1.
DR Pfam; PF00310; GATase_2; 1.
DR TIGRFAMs; TIGR01536; asn_synth_AEB; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
KW Ligase.
SQ SEQUENCE 579 AA; 65231 MW; B6E7B7902DF2BC95 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 579;
Best Local Similarity 34.4%; Pred. No. 1.2e+02;
Matches 1; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

QY 1 VDQGK-----ATNIPPYTPAGTK 18
DB 462 IDGLKAHAEKHVTDRLMLNANIFFPNTPTTK 493

RESULT 13
Q9SM55 PHAVU PRELIMINARY; PRT; 579 AA.
AC Q9SM55;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.

DE Asparagine synthetase (Type-I) (EC 6.3.5.4).

GN Nameas1;

OS Phaseolus vulgaris (Kidney bean) (French bean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

OC Phaseolus.

OX NCBI_TaxID=3885;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Great Northern; TISSUE=Root;

RA Galvez-Valdivieso G., Osuna D., Perez-Vicente R., Pineda M.,

RA Aguilar M.;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

CC -----

CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; AJ133522; CAB57292.1; -; mRNA.

DR HSP; P22106; 1CT9.

DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.

DR GO; GO:0016874; F:ligase activity; IEA.

DR GO; GO:0006529; P:asparagine biosynthesis; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR006426; Asn_synth_AEB.

DR InterPro; IPR001962; Asn_synthase.

DR InterPro; IPR000583; GATase_2.

DR Pfam; PF00733; Asn_synthase; 1.

DR Pfam; PF00310; GATase_2; 1.

DR TIGRFAMs; TIGR01536; asn_synth_AEB; 1.

DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.

KW Ligase.

FT CHAIN 579 AA; 65266 MW; 7A74F5A8E52CE2B6 CRC64;

SQ SEQUENCE

Query Match 47.4%; Score 46; DB 2; Length 579;

Best Local Similarity 34.4%; Pred. No. 1.2e+02;

Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQK-----ATNIFPYTAPGK 18

Db 462 IDGLKHAERKHTVDRMLNANIPFNTPTTK 493

RESULT 14

ASNS2 LOTJA

ID ASNS2 LOTJA STANDARD; PRT; 585 AA.

AC P49093;

DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.

DT 01-FEB-1996, sequence version 39.

DT 07-FEB-2006, entry version 1.

DE Asparagine synthetase [glutamine-hydrolyzing] 2 (EC 6.3.5.4)

DE (Glutamine-dependent asparagine synthetase 2).

GN Name=AS2;

OS Lotus japonicus.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

OX NCBI_TaxID=34305;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC STRAIN=cv. Gifu / B-129;

RX MEDLINE=96270368; PubMed=8639748;

RA Waterhouse R.N., Smyth A.J., Massoneau A., Prosser I.M.,

RA Clarkson D.T.;

RT "Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus: dynamics of asparagine synthesis in N-sufficient conditions".;

RL Plant Mol. Biol. 30:883-897(1996).

CC -!- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP +

CC phosphate + L-asparagine + L-glutamate.

CC -!- PATHWAY: Asparagine biosynthesis.

CC -!- SIMILARITY: Contains 1 asparagine synthetase domain.

CC -!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.

CC -----

CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; X89410; CAA61590.1; -; mRNA.

DR PIR; S69183; S69183.

DR HSP; P22106; 1CT9.

DR InterPro; IPR006426; Asn_synth_AEB.

DR InterPro; IPR001962; Asn_synthase.

DR InterPro; IPR000583; GATase_2.

DR Pfam; PF00733; Asn_synthase; 1.

DR Pfam; PF00310; GATase_2; 1.

DR TIGRFAMs; TIGR01536; asn_synth_AEB; 1.

DR PROSITE; PS00443; GATASE_TYPE_II; 1.

KW Amino-acid biosynthesis; Asparagine biosynthesis;

KW Glutamine amidotransferase; Ligase.

FT INIT MET 0 By similarity.

FT CHAIN 1 585 Asparagine synthetase (glutamine-hydrolyzing) 2.

FT FTID-PRO 0000056923.

FT DOMAIN 192 515 Asparagine synthetase.

FT REGION 1 107 Glutamine amidotransferase.

FT ACT_SITE 1 1 GATase (By similarity).

SQ SEQUENCE 585 AA; 65839 MW; F56DCA2015F73451 CRC64;

Query Match 47.4%; Score 46; DB 1; Length 585;

Best Local Similarity 31.2%; Pred. No. 1.2e+02;

Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;

Qy 1 VDQK-----ATNIFPYTAPGK 18

Db 461 IDGLKHAERKHTVDRMLNANIPFNTPTTK 492

RESULT 15

O8CKM1 YERPE

ID O8CKM1 YERPE PRELIMINARY; PRT; 641 AA.

AC O8CKM1;

DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2003, sequence version 1.

DT 07-FEB-2006, entry version 12.

DE Hypothetical.

GN OrderedLocusNames=Y3288;

OS Yersinia pestis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Yersinia.

OX NCBI_TaxID=632;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=KIM5 / Biovar Mediaevalis;

RX MEDLINE=22137863; PubMed=12142430;

RX DOI=10.1128/JB.184.16.4601-4611.2002;

RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,

RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

RA Perry R.D.;

RT "Genome sequence of Yersinia pestis KIM.";

RL J. Bacteriol. 184:4601-4611(2002).

CC -----

CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; AE013929; AAM86837.1; -; Genomic_DNA.

DR BioCyc; YPES187410.Y3288-MONOMER; -.

DR GO; GO:0019867; C:outer membrane; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR008640; Hep_Hag.

DR InterPro; IPR008635; HIM.

DR InterPro; IPR005594; Yada_C.

DR Pfam; PF05658; Hep_Hag; 7.

DR Pfam; PF05662; HIM; 4.

DR Pfam; PF03895; Yada; 1.

KW Hypothetical protein.

SQ SEQUENCE 641 AA; 62094 MW; A595153FEE45162 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 641;

Best Local Similarity 52.9%; Pred. No. 1.3e+02;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAGT 17

Db ::::: | |

82 LMGQKATNLAPATISST 98

Search completed: August 30, 2006, 04:29:13

Job time : 74.1818 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 17.8182 Seconds
(without alignments)
88.424 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97

Sequence: 1 VDCQKATNIPPTAPGPK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /EMC_Celerra_SID3S/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SID3S/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SID3S/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SID3S/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SID3S/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SID3S/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SID3S/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	108	2	US-09-281-760E-35
2	97	100.0	312	2	US-09-701-623C-2
3	97	100.0	426	1	US-08-336-583-2
4	97	100.0	426	5	PCT-US95-13795-2
5	87	89.7	431	2	US-09-479-614-14
6	87	89.7	496	2	US-09-479-614-2
7	87	89.7	496	2	US-09-479-614-29
8	73	75.3	343	2	US-09-401-636-7
9	58	59.8	341	2	US-09-401-636-3
10	58	59.8	341	2	US-09-401-636-4
11	58	59.8	341	2	US-09-401-636-6
12	58	59.8	341	2	US-09-401-636-9
13	58	59.8	341	2	US-09-401-636-11
14	58	59.8	342	2	US-09-401-636-5
15	58	59.8	342	2	US-09-401-636-8
16	58	59.8	345	2	US-09-401-636-10
17	46	47.4	135	2	US-09-252-991A-30004
18	46	47.4	497	2	US-10-077-699C-5
19	45	46.4	350	2	US-09-094-103-6
20	45	46.4	350	2	US-09-080-963-2
21	45	46.4	350	2	US-08-947-251-2
22	45	46.4	350	2	US-09-769-787-89
23	45	46.4	358	2	US-09-583-110-5009
24	45	46.4	358	2	US-09-107-433-2960
25	45	46.4	583	7	5256558-4
26	44	45.4	121	2	US-09-710-279-2524

Sequence 2524, Ap

Sequence 5009, Ap

Patent No. 5256558

Sequence 2524, Ap

27	44	45.4	132	2	US-09-134-001C-4212
28	43	44.3	475	2	US-08-840-767-10
29	43	44.3	586	7	5256558-2
30	42	43.3	557	2	US-09-902-540-12884
31	42	43.3	985	2	US-09-993-777-6
32	42	43.3	985	2	US-09-993-777-66
33	42	43.3	985	2	US-09-994-064-6
34	42	43.3	985	2	US-09-994-064-66
35	42	43.3	985	5	PCT-US96-03916-6
36	42	43.3	985	5	PCT-US96-03916-66
37	41	42.3	232	2	US-09-489-039A-8106
38	41	42.3	570	1	US-08-967-364-1
39	41	42.3	570	1	US-08-967-364-7
40	41	42.3	570	2	US-09-368-408-1
41	41	42.3	570	2	US-09-368-408-7
42	41	42.3	1364	2	US-09-252-991A-26880
43	40.5	41.8	464	2	US-09-543-681A-4924
44	40.5	41.8	608	2	US-09-252-991A-27624
45	40	41.2	63	2	US-09-612-402B-29

ALIGNMENTS

RESULT 1

US-09-281-760E-35
; Sequence 35, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; PRIOR FILING DATE: 1999-03-30
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81)..(81)
; OTHER INFORMATION: The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly,
; OTHER INFORMATION: Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82)..(82)
; OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (460)..(462)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (500)..(500)

OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (5307)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (8537)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1832)..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid

US-09-281-760E-35

Query Match 100.0%; Score 97; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIFPYTAPGTK 18
|||||

Db 47 VDGOKATNIFPYTAPGTK 64
|||||

RESULT 2

US-09-701-623C-2
Sequence 2, Application US/09701623C
Patent No. 6811782
GENERAL INFORMATION:
APPLICANT: Wang Ph.D., Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY
FILE REFERENCE: 11514153US1
CURRENT APPLICATION NUMBER: US/09/701,623C
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2

LENGTH: 312

TYPE: PRT

ORGANISM: Dog

FEATURE:

OTHER INFORMATION: CH2CH3n of dog IgE

PUBLICATION INFORMATION:

AUTHORS: Patel,

JOURNAL: Immunogenetics

VOLUME: 41

PAGES: 282-286

DATE: 1995

US-09-701-623C-2

Query Match 100.0%; Score 97; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIFPYTAPGTK 18
|||||

Db 48 VDGOKATNIFPYTAPGTK 65

RESULT 3

US-08-336-583-2
Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-336-583-2

Query Match 100.0%; Score 97; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIFPYTAPGTK 18
|||||

Db 146 VDGOKATNIFPYTAPGTK 163
|||||

RESULT 4

PCT-US95-13795-2
Sequence 2, Application PC/TUS9513795
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match      100.0%; Score 97; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGPK 18
Db      146 VDGQKATNIPFYTAGPK 163

RESULT 5
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match      89.7%; Score 87; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      151 VDGQKATNIPFYTAGP 166

RESULT 6
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match      89.7%; Score 87; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      216 VDGQKATNIPFYTAGP 231

RESULT 7
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match      89.7%; Score 87; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      216 VDGQKATNIPFYTAGP 231

RESULT 8
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-7

Query Match      75.3%; Score 73; DB 2; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.00086;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 15
```

```
Db      61 VDGQKATNIPFYP 75
||||| |:|||||
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYP 13
||||| |:|||||
Db      62 VDGQKATNIPFYP 74

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYP 13
||||| |:|||||
Db      62 VDGQKATNIPFYP 74

RESULT 13
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYP 13
||||| |:|||||
Db      62 VDGQKATNIPFYP 74

RESULT 10
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYP 13
||||| |:|||||
Db      62 VDGQKATNIPFYP 74

RESULT 11
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
```

; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match 59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYT 13
Db 62 VDQGEAENLFYPT 74

RESULT 14

US-09-401-636-5
; Sequence 5, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-5

Query Match 59.8%; Score 58; DB 2; Length 342;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYT 13
Db 62 VDQGEAENLFYPT 74

RESULT 15

US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match 59.8%; Score 58; DB 2; Length 342;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYT 13
Db 62 VDQGEAENLFYPT 74

Search completed: August 30, 2006, 04:33:01
Job time : 18.8182 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 90.9091 Seconds
(without alignments)
91.717 Million cell updates/sec

Title: US-10-758-165a-9
Perfect score: 97
Sequence: 1 VDGQKATNIPFYTAGTK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-9
2	97	100.0	312	5	US-10-723-207-2
3	97	100.0	426	4	US-10-214-524-28
4	87	89.7	18	5	US-10-758-165-10
5	87	89.7	431	3	US-09-479-614-14
6	87	89.7	431	4	US-10-409-772-14
7	87	89.7	496	3	US-09-479-614-2
8	87	89.7	496	3	US-09-479-614-29
9	87	89.7	496	4	US-10-214-524-25
10	87	89.7	496	4	US-10-409-772-2
11	87	89.7	496	4	US-10-409-772-29
12	73	75.3	343	3	US-09-401-636-7
13	73	75.3	343	4	US-10-176-664-7
14	73	75.3	343	4	US-10-673-594-7
15	73	75.3	577	4	US-10-214-524-29
16	58	59.8	337	4	US-10-438-794-3
17	58	59.8	337	4	US-10-453-915-3
18	58	59.8	338	4	US-10-438-794-6
19	58	59.8	338	4	US-10-453-915-6
20	58	59.8	341	3	US-09-401-636-3
21	58	59.8	341	3	US-09-401-636-4
22	58	59.8	341	3	US-09-401-636-6
23	58	59.8	341	3	US-09-401-636-9
24	58	59.8	341	3	US-09-401-636-11
25	58	59.8	341	4	US-10-176-664-3
26	58	59.8	341	4	US-10-176-664-4
27	58	59.8	341	4	US-10-176-664-6

28	58	59.8	341	4	US-10-176-664-9	Sequence 9, Appli
29	58	59.8	341	4	US-10-176-664-11	Sequence 11, Appli
30	58	59.8	341	4	US-10-673-594-3	Sequence 3, Appli
31	58	59.8	341	4	US-10-673-594-4	Sequence 4, Appli
32	58	59.8	341	4	US-10-673-594-6	Sequence 6, Appli
33	58	59.8	341	4	US-10-673-594-9	Sequence 9, Appli
34	58	59.8	341	4	US-10-673-594-11	Sequence 11, Appli
35	58	59.8	342	3	US-09-401-636-5	Sequence 5, Appli
36	58	59.8	342	3	US-09-401-636-8	Sequence 8, Appli
37	58	59.8	342	4	US-10-176-664-5	Sequence 5, Appli
38	58	59.8	342	4	US-10-176-664-8	Sequence 8, Appli
39	58	59.8	342	4	US-10-673-594-5	Sequence 5, Appli
40	58	59.8	342	4	US-10-673-594-8	Sequence 8, Appli
41	58	59.8	345	3	US-09-401-636-10	Sequence 10, Appli
42	58	59.8	345	4	US-10-176-664-10	Sequence 10, Appli
43	58	59.8	345	4	US-10-673-594-10	Sequence 10, Appli
44	58	59.8	347	4	US-10-438-794-14	Sequence 14, Appli
45	58	59.8	347	4	US-10-453-915-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match 100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGTK 18
| | | | | | | | | | | | | | | | | |
Db 1 VDGQKATNIPFYTAGTK 18

RESULT 2
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2


```
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
Query Match      89.7%; Score 87; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAPG 16
Db      216 VDGOKATNIPPYTAPG 231

RESULT 8
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29
Query Match      89.7%; Score 87; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAPG 16
Db      216 VDGOKATNIPPYTAPG 231

RESULT 9
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61

; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/115,033
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
Query Match      89.7%; Score 87; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAPG 16
Db      216 VDGOKATNIPPYTAPG 231

RESULT 11
US-10-409-772-29
; Sequence 29, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
Query Match      89.7%; Score 87; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAPG 16
Db      216 VDGOKATNIPPYTAPG 231

RESULT 10
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2
Query Match      89.7%; Score 87; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAPG 16
Db      216 VDGOKATNIPPYTAPG 231

RESULT 11
US-10-409-772-29
; Sequence 29, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
Query Match      89.7%; Score 87; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIPPYTAPG 16
Db      216 VDGOKATNIPPYTAPG 231
```

```
Db      216 VDGQKATNIPFYTAP 231

RESULT 12
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-7

Query Match      75.3%; Score 73; DB 3; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAP 15
      ||||| :|||
Db      61 VDGQKAENLFFYTAP 75

RESULT 13
US-10-176-664-7
; Sequence 7, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7

Query Match      75.3%; Score 73; DB 4; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAP 15
      ||||| :|||
Db      61 VDGQKAENLFFYTAP 75

RESULT 14
US-10-673-594-7
; Sequence 7, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7

Query Match      75.3%; Score 73; DB 4; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAP 15
      ||||| :|||
Db      295 VDGQKAENLFFYTAP 309

Search completed: August 30, 2006, 05:13:00
Job time : 91.9091 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 9.27273 Seconds
(without alignments)
133.695 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97

Sequence: 1 VDGQKATNIFPYTPGTK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SID33/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 2: /EMC_Celerra_SID33/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SID33/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /EMC_Celerra_SID33/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 5: /EMC_Celerra_SID33/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 6: /EMC_Celerra_SID33/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SID33/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SID33/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	47.4	80	7	US-11-330-403-2450
2	46	47.4	239	7	US-11-330-403-3689
3	46	47.4	250	7	US-11-330-403-15600
4	46	47.4	287	7	US-11-330-403-17777
5	46	47.4	579	7	US-11-330-403-2402
6	46	47.4	579	7	US-11-330-403-6386
7	46	47.4	579	7	US-11-330-403-11285
8	46	47.4	579	7	US-11-330-403-18232
9	46	47.4	581	7	US-11-330-403-1293
10	46	47.4	586	7	US-11-330-403-4518
11	45.5	46.9	581	7	US-11-330-403-7358
12	45	46.4	64	7	US-11-375-095-104
13	45	46.4	583	7	US-11-330-403-13229
14	45	46.4	583	7	US-11-330-403-14971
15	44	45.4	584	7	US-11-330-403-5521
16	44	45.4	586	7	US-11-330-403-482
17	43	44.3	254	6	US-10-471-571A-726
18	43	44.3	586	7	US-11-330-403-10108
19	43	44.3	586	7	US-11-330-403-14969
20	42.5	43.8	236	7	US-11-375-221-16
21	42	43.3	585	7	US-11-330-403-13141
22	42	43.3	644	7	US-11-330-403-6482
23	42	43.3	644	7	US-11-330-403-15095
24	42	43.3	985	7	US-11-342-171-6
25	42	43.3	985	7	US-11-342-171-66

26 41.5 42.8 582 7 US-11-330-403-14312 Sequence 14312, A
27 41.5 42.8 582 7 US-11-330-403-15230 Sequence 15230, A
28 41 42.3 570 6 US-10-511-937-2612 Sequence 2612, Ap
29 40.5 41.8 582 7 US-11-330-403-15597 Sequence 15597, A
30 40 41.2 189 7 US-11-330-403-12759 Sequence 12759, A
31 40 41.2 332 7 US-11-056-355B-11318 Sequence 11318, A
32 40 41.2 339 6 US-10-449-902-30393 Sequence 30393, A
33 40 41.2 339 6 US-10-449-902-36927 Sequence 36927, A
34 40 41.2 339 6 US-10-449-902-51715 Sequence 51715, A
35 40 41.2 339 7 US-11-056-355B-11317 Sequence 11317, A
36 40 41.2 377 7 US-11-056-355B-11316 Sequence 11316, A
37 40 41.2 422 6 US-10-953-349-22933 Sequence 22933, A
38 40 41.2 422 6 US-11-056-355B-54494 Sequence 54494, A
39 40 41.2 451 6 US-10-953-349-49331 Sequence 49331, Ap
40 41.2 451 7 US-11-056-355B-35016 Sequence 35016, A
41 40 41.2 451 7 US-11-056-355B-101754 Sequence 101754, A
42 40 41.2 451 7 US-11-056-355B-112993 Sequence 112993, A
43 40 41.2 467 6 US-10-953-349-22932 Sequence 22932, A
44 40 41.2 467 7 US-11-056-355B-54493 Sequence 54493, A
45 40 41.2 469 6 US-10-953-349-4930 Sequence 4930, Ap

ALIGNMENTS

RESULT 1

US-11-330-403-2450
; Sequence 2450, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 2450
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-2450

Query Match 47.4%; Score 46; DB 7; Length 80;
Best Local Similarity 34.4%; Pred. No. 0.93;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

QY 1 VDGOK-----ATNIFPYTPGTK 18
|||
Db 27 IDGLKAHAEKHVTRMLNANIPFNTPTTK 58
|||

RESULT 2

US-11-330-403-3689
; Sequence 3689, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 3689
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(239)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-3689

Query Match 47.4%; Score 46; DB 7; Length 239;

```
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-2402

Query Match      47.4%; Score 46; DB 7; Length 579;
Best Local Similarity 34.4%; Pred. No. 8;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIPFYTAGTK 18
: || |
Db 131 IDGLKAHAKEHVTDRLMLNAANIPFNTPTTK 162
: || |

RESULT 3
US-11-330-403-15600
; Sequence 15600, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15600
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-15600

Query Match      47.4%; Score 46; DB 7; Length 250;
Best Local Similarity 34.4%; Pred. No. 3.2;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIPFYTAGTK 18
: || |
Db 131 IDGLKAHAKEHVTDRLMLNAANIPFNTPTTK 162
: || |

RESULT 4
US-11-330-403-17777
; Sequence 17777, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 17777
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-17777

Query Match      47.4%; Score 46; DB 7; Length 287;
Best Local Similarity 34.4%; Pred. No. 3.7;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDQOK-----ATNIPFYTAGTK 18
: || |
Db 170 IDGLKAHAKEHVTDRLMLNAANIPFNTPTTK 201
: || |

RESULT 5
US-11-330-403-2402
; Sequence 2402, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 2402
; LENGTH: 579
; FILE REFERENCE: 38-21(53629)B
```

; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 18232
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-18232

Query Match 47.4%; Score 46; DB 7; Length 579;
Best Local Similarity 34.4%; Pred. No. 8;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDGQK-----ATNIPFPYTPGK 18
: || |
Db 462 IDGLKAHAEKHVTDRLMLNAANIPFNTPTTK 493

RESULT 9

US-11-330-403-1293
; Sequence 1293, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 1293
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(581)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-1293

Query Match 47.4%; Score 46; DB 7; Length 581;
Best Local Similarity 34.4%; Pred. No. 8;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Qy 1 VDGQK-----ATNIPFPYTPGK 18
: || |
Db 463 IDGLKAHAEKHVTDRLMLNAANIPFNTPTTK 494

RESULT 10

US-11-330-403-4518
; Sequence 4518, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4518
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Lotus corniculatus var. japonicus
US-11-330-403-4518

Query Match 47.4%; Score 46; DB 7; Length 586;
Best Local Similarity 31.2%; Pred. No. 8.1;
Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;

Qy 1 VDGQK-----ATNIPFPYTPGK 18
: || |
Db 462 IDGLKAHAEKHVTDRLMLNAANIPFNTPTTK 493

RESULT 11
US-11-330-403-7358
; Sequence 7358, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 7358
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(581)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-7358

Query Match 46.9%; Score 45.5; DB 7; Length 581;
Best Local Similarity 33.3%; Pred. No. 9.7;
Matches 11; Conservative 2; Mismatches 5; Indels 15; Gaps 1;

Qy 1 VDGQK-----ATNIPFPYTPGK 18
: || |
Db 462 IDGLKAHAEKHVTDRLMLNAANIPFNTPTTK 494

RESULT 12

US-11-375-095-104
; Sequence 104, Application US/11375095
; Publication No. US20060156443A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: MENENDEZ-HUMARA, JAIME
; APPLICANT: VAN, HUA
; APPLICANT: RICHARD, CRAIG
; APPLICANT: BRINKHOFF, W. LEIGH
; APPLICANT: SWORDS, KATHY M. M.
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0162
; CURRENT APPLICATION NUMBER: US/11/375,095
; CURRENT FILING DATE: 2006-03-15
; PRIOR APPLICATION NUMBER: US/10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 104
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-375-095-104

Query Match 46.4%; Score 45; DB 7; Length 64;
Best Local Similarity 72.7%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 NIPFPYTPGK 18
: || |
Db 10 NIMPYPFGTK 20

RESULT 13
US-11-330-403-13229
; Sequence 13229, Application US/11330403

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:15:52 ; Search time 65.4545 Seconds
(without alignments)
125.735 Million cell updates/sec

Title: US-10-758-165a-10
Perfect score: 97
Sequence: 1 VDGQKATNIFYPAGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	ADR10610	Cat Ige e
2	97	100.0	431	ADG73237	Adg73237 Cat immun
3	97	100.0	496	ABP96580	Abp96580 Cat Ige h
4	97	100.0	496	ABU09338	Abu09338 Feline Ig
5	97	100.0	496	ABU09336	Abu09336 Feline Ig
6	97	100.0	496	ADG73251	Adg73251 Cat parti
7	97	100.0	496	ADG73225	Adg73225 Cat parti
8	87	89.7	18	ADR10609	Adr10609 Dog Ige e
9	87	89.7	312	AAW79995	Aaw79995 Dog immun
10	87	89.7	417	AAW23067	Aaw23067 Canine Ig
11	87	89.7	426	AAW97753	Aaw97753 Canine Ig
12	87	89.7	426	ABP96583	Abp96583 Dog Ige h
13	77	79.4	577	ABP96584	Abp96584 Duckbille
14	72	74.2	343	3 AAB06204	Aab06204 Platypus
15	60	61.9	337	8 ADF90022	Adf90022 Opossum-r
16	60	61.9	337	8 ADN0643	Adn0643 ORO prote
17	60	61.9	338	8 ADF90025	Adf90025 Opossum-h
18	60	61.9	338	8 ADN0646	Adn0646 OSO prote
19	60	61.9	341	3 AAB06206	Aab06206 Immunogen
20	60	61.9	341	3 AAB03644	Aab03644 Opossum I
21	60	61.9	341	3 AAB06208	Aab06208 Immunogen
22	60	61.9	342	3 AAB06205	Aab06205 Immunogen
23	60	61.9	345	3 AAB06207	Aab06207 Immunogen

24	60	61.9	347	8 ADF90033	Adf90033 Opossum-h
25	60	61.9	347	8 ADN00654	Adn00654 OSO-H pro
26	60	61.9	353	8 ADN00661	Adn00661 H-OCO-H p
27	60	61.9	427	6 ABP96591	Abp96591 Brushtail
28	60	61.9	446	6 ABP96587	Abp96587 Opossum I
29	60	61.9	555	8 ADF90027	Adf90027 Opossum-r
30	60	61.9	555	8 ADN00648	Adn00648 ORO pro
31	60	61.9	557	8 ADF90031	Adf90031 Opossum-h
32	60	61.9	557	8 ADF90035	Adf90035 Opossum-h
33	60	61.9	557	8 ADN00656	Adn00656 OSO pro
34	60	61.9	557	8 ADN00652	Adn00652 modOSO
35	60	61.9	566	8 ADF90029	Adf90029 Opossum-h
36	60	61.9	566	8 ADF90037	Adf90037 Opossum-h
37	60	61.9	566	8 ADN00658	Adn00658 OSO-H p
38	60	61.9	566	8 ADN00650	Adn00650 modOSO-H
39	55	56.7	18	8 ADR10612	Adr10612 Sheep Ige
40	55	56.7	341	3 AAB06202	Aab06202 Immunogen
41	55	56.7	342	3 AAB06201	Aab06201 Immunogen
42	55	56.7	567	6 ABP96588	Abp96588 Pig Ige h
43	44	45.4	87	3 AAY83167	Aay83167 PAGE1 pool
44	44	45.4	99	7 ADG42685	Adg42685 Human PAG
45	44	45.4	99	7 ADJ55754	Adj55754 Peptide h

ALIGNMENTS

RESULT 1
ADRI0610
ID ADR10610 standard; peptide; 18 AA.
XX ADR10610;
XX
DT 21-OCT-2004 (first entry)
DE Cat Ige epitope recognised by monoclonal antibody 3.76, SEQ ID 10.
XX
XX Antiasthmatic; Antiallergic; Immunosuppressive; Ige; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
cat.
XX
XX Felis catus.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PP 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hammerberg B;
XX WPI; 2004-593545/57.
XX
PT Novel antibody that specifically binds to mammalian Ige epitope, useful
for testing an allergen reactivity of Ige sample, detecting mammalian Ige
or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
specifically binds to a mammalian Ige epitope, where the epitope is
between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige.
XX (I) is useful for testing an allergen reactivity of an Ige sample. The
allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
and corn allergens. The sample is a biological sample collected from a
dog, cat or horse. (I) is also useful for detecting mammalian Ige and for
treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
antibodies recognise epitopes on canine Ige corresponding to amino acid
residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE. The present sequence is the
CC cat IgE 3.76 recognition site.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGKQ 18
| | | | | | | | | | | | | | | | | |
Db 1 VDGQKATNIFPYTAPGKQ 18

RESULT 2
ADG73237
ID ADG73237 standard; protein; 431 AA.

XX AC ADG73237;
XX DT 11-MAR-2004 (first entry)
XX XX

XX Cat immunoglobulin E (IgE) constant region.

XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
XX immune response; IgE-mediated response; allergy; cat; constant region.
XX
XX Felis catus.

XX US2003216565-A1.

XX 20-NOV-2003.

XX 07-APR-2003; 2003US-00409772.

XX 07-JAN-1999; 99US-0115033P.

XX 07-JAN-2000; 2000US-00479614.

XX (MCCA/) MCCALL C.

XX (WEBE/) WEBER E.

XX McCall C, Weber E;

XX WPI; 2004-010802/01.

XX N-PSDB; ADG73236.

XX New isolated nucleic acid molecule encoding a portion of a feline IgE
XX heavy chain protein, useful for treating and/or eliciting feline immune
XX responses for IgE-mediated responses, such as allergies.

XX Claim 12; SEQ ID NO 14; 44pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX portion of a feline IgE heavy chain protein. The methods and compositions
XX of the present invention are useful for eliciting feline immune responses
XX for and/or treating IgE-mediated responses, such as allergies. This is
XX the amino acid sequence of a cat immunoglobulin E (IgE) constant region.

XX Sequence 431 AA;

Query Match 100.0%; Score 97; DB 8; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGKQ 18
| | | | | | | | | | | | | | | | | |
Db 151 VDGQKATNIFPYTAPGKQ 168

RESULT 3

ABP96580

ID ABP96580 standard; protein; 496 AA.

XX AC ABP96580;

XX DT 28-MAY-2003 (first entry)

XX Cat IgE heavy chain amino acid sequence SEQ ID NO:25.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
XX dermatological; antiinflammatory; IgE-mediated condition; food allergy;
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX urticaria hives.

XX Felis catus.

XX W02003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) ICE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
XX against IgE, by identifying peptide eliciting CTL response to IgE
XX peptides naturally presented by major histocompatibility complex class I
XX protein.

XX Example 7; Page 145-147; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides
XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
XX E (IgE), comprising providing a test peptide (T) suspected of being able
XX to bind to major histocompatibility complex (MHC) class I molecule, and
XX evaluating (T) for ability to elicit in a mammal a CTL response to
XX naturally processed and presented IgE peptides, where a peptide that
XX induces such a response is identified. Also described are compositions:
XX (C1) comprising at least one immunogenic peptide (I) identified by (M1);
XX (C2) comprising at least one isolated polynucleotide encoding (I); and
XX (C3) comprising antigen-presenting cells that recognise at least one (I).
XX Where C1-3 are able to bind to at least one MHC class I molecule and to
XX elicit in a mammal a CTL response to naturally processed and presented
XX IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,
XX vasotropic, dermatological, antiinflammatory and cytostatic activities,
XX and can be used as inducers of a CTL response against IgE, and in
XX vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
XX mammal. C1-3 are useful for modulating an IgE-mediated condition such as
XX IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
XX hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
XX useful for treating atopic hypersensitivity conditions (such as allergic
XX rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
XX atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
XX hives). The present sequence represents an IgE heavy chain amino acid
XX sequence, which is given in an example from the present invention

XX Sequence 496 AA;

Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGKQ 18

```

Db      216 VDGQKATNIFPYTAPGKQ 233
|||||
RESULT 4
ABU09338
ID ABU09338 standard; protein; 496 AA.
XX
AC ABU09338;
XX
DT 27-JUN-2003 (first entry)
XX
DE Feline IgE epsilon heavy chain #2.
XX
KW Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
KW IgE-mediated immune response; allergy; neoplasia; vaccine technology;
KW antibody technology; antiallergic; antiparasitic; cytostatic.
XX
OS Felis catus.
XX
PN US2003013183-A1.
XX
PD 16-JAN-2003.
XX
PF 07-JAN-2000; 2000US-00479614.
XX
PR 07-JAN-1999; 99US-0115033P.
XX
PA (MCCA/) MCCALL C.
PA (WEBE/) WEBER E.
XX
PI McCall C, Weber E;
XX
DR WPI; 2003-391997/37.
DR N-PSDB; ABX95715.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
PS Claim 1; Page 37-39; 45pp; English.
XX
CC The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #2
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGQKATNIFPYTAPGKQ 18
|||||
Db      216 VDGQKATNIFPYTAPGKQ 233
|||||
RESULT 5
ABU09336
ID ABU09336 standard; protein; 496 AA.
XX
AC ABU09336;
XX
DT 27-JUN-2003 (first entry)
XX
DE Feline IgE epsilon heavy chain #1.
XX
KW Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
KW antibody technology; antiallergic; antiparasitic; cytostatic.
XX
OS Felis catus.
XX
PN US2003013183-A1.
XX
PD 16-JAN-2003.
XX
PF 07-JAN-2000; 2000US-00479614.
XX
PR 07-JAN-1999; 99US-0115033P.
XX
PA (MCCA/) MCCALL C.
PA (WEBE/) WEBER E.
XX
PI McCall C, Weber E;
XX
DR WPI; 2003-391997/37.
DR N-PSDB; ABX95713.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
PS Claim 1; Page 24-25; 45pp; English.
XX
CC The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #1
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGQKATNIFPYTAPGKQ 18
|||||
Db      216 VDGQKATNIFPYTAPGKQ 233
|||||
RESULT 6
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
AC ADG73251;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cat partial immunoglobulin E (IgE) heavy chain #2.
XX
KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
KW immune response; IgE-mediated response; allergy; cat; heavy chain.

```

```

KW IgE-mediated immune response; allergy; neoplasia; vaccine technology;
KW antibody technology; antiallergic; antiparasitic; cytostatic.
XX
OS Felis catus.
XX
PH Location/Qualifiers
FT Key 66..496
FT Region /note= "This sequence is given as SEQ ID No:14 and is
FT specifically claimed in Claim 12"
FT 284..309
FT Region /note= "This sequence is given as SEQ ID No:11 and is
FT specifically claimed in Claim 9"
FT 288..305
FT Region /note= "This sequence is given as SEQ ID No:8 and is
FT specifically claimed in Claim 10"
FT 291..302
FT Region /note= "This sequence is given as SEQ ID No:5 and is
FT specifically claimed in Claim 11"
XX
XX US2003013183-A1.
PN
XX
XX 16-JAN-2003.
PD
XX
XX 07-JAN-2000; 2000US-00479614.
PF
XX
XX 07-JAN-1999; 99US-0115033P.
PR
XX
XX (MCCA/) MCCALL C.
PA
PA (WEBE/) WEBER E.
XX
XX McCall C, Weber E;
PI
XX
XX WPI; 2003-391997/37.
DR
DR N-PSDB; ABX95713.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IgE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
PS Claim 1; Page 24-25; 45pp; English.
XX
CC The present invention relates to the isolation of feline immunoglobulin E
CC (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IgE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IgE and its functions. The
CC present sequence represents feline IgE epsilon heavy chain #1
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGQKATNIFPYTAPGKQ 18
|||||
Db      216 VDGQKATNIFPYTAPGKQ 233
|||||
RESULT 6
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
AC ADG73251;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cat partial immunoglobulin E (IgE) heavy chain #2.
XX
KW antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
KW immune response; IgE-mediated response; allergy; cat; heavy chain.

```


CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE.
XX
SQ Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAPG 16
| | | | | | | | | | | | | | | |
Db 1 VDGQKATNIPFYTAPG 16

RESULT 9
AAV79995
ID AAV79995 standard; protein; 312 AA.
XX
AC AAV79995;
XX
DT 15-MAY-2000 (first entry)
XX
DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
XX
KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS Canis sp.
XX
PN WO9967293-A1.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013959.
XX
PR 20-JUN-1998; 98US-00100287.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY, Walfield AM;
XX
WPI; 2000-160578/14.
XX
PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy.
XX
PS Example 1; Page 66-68; 155pp; English.
XX
CC The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
CC a target effector site on the epsilon-heavy chain of IgE, and so
CC preventing triggering and activation of mast cells and basophils and
CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe (non-
CC anaphylactogenic) antibodies. AAV79994 to AAY80084 represent amino acid
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 312 AA;

Query Match 89.7%; Score 87; DB 3; Length 312;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAPG 16
| | | | | | | | | | | | | | | |
Db 48 VDGQKATNIPFYTAPG 63

RESULT 10
AAW23067
ID AAW23067 standard; protein; 417 AA.
XX
AC AAW23067;
XX
DT 30-JUN-2005 (revised)
DT 16-JUN-2005 (revised)
DT 19-FEB-1998 (first entry)
XX
DE Canine IgE heavy chain constant region (exon 1-4 product).
XX
KW IgE; immunoglobulin; antibody; heavy chain constant region; allergy;
KW hypersensitivity; therapy; dog; antisense; immunomodulation.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 55 /note= "encoded by ACC"
FT Misc-difference 56 /note= "encoded by TAC"
FT Misc-difference 67 /note= "encoded by GCC"
FT Misc-difference 83 /note= "encoded by NNT"
FT Misc-difference 174 /note= "encoded by GGN"
FT Misc-difference 175 /note= "encoded by NNG"
FT Misc-difference 176 /note= "encoded by TGN"
FT Misc-difference 203 /note= "encoded by TCC"
FT Misc-difference 204 /note= "encoded by GAC"
XX
PN WO9730156-A2.
XX
PD 21-AUG-1997.
XX
PF 14-FEB-1997; 97WO-US002322.
XX
PR 14-FEB-1996; 96US-00601197.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Mermer B, Harris RA, Siefring AE;
XX
WPI; 1997-425031/39.
XX
N-PSDB; AAT79278.
XX
PT Isolated canine IgE heavy chain constant region DNA - useful to develop
PT products for treatment of canine allergies and for immunomodulation in
PT dogs.
XX
PS Disclosure; Page 35-39; 59pp; English.
XX
CC This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE
CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
CC peptides encoded by exons 1-6 can be produced in eukaryotic or
CC prokaryotic cells. Such peptides, and antibodies raised against them, are
CC used in methods to treat the manifestation of allergy in dogs, e.g. to
CC treat Type I immediate hypersensitivity, and for immunomodulation

```
CC Revised record issued on 30-JUN-2005 : Typo in comments
XX
SQ Sequence 417 AA;

Query Match      89.7%; Score 87; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPG 16
Db 141 VDGQKATNIFPYTAPG 156

RESULT 11
AAR97753
ID AAR97753 standard; protein; 426 AA.
XX
AC AAR97753;
XX
DT 28-AUG-1996 (first entry)
XX
DE Canine IgE.
XX
KW IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX
OS Canis familiaris.
XX
PN WO9614867-A1.
XX
PD 23-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US013795.
XX
PR 09-NOV-1994; 94US-00336583.
XX
PR 09-NOV-1994; 94US-00336891.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Hollis GF, Patel MD;
XX
DR WPI; 1996-277321/28.
DR N-PSDB; AAT29824.
XX
New DNA encoding canine IgE and IgA - useful in vaccines, anti-sense
therapy, assays, drug screening, etc.
XX
PS Claim 11; Page 29-30; 49pp; English.
XX
The canine IgE amino acid sequence (AAR97753) was deduced from an
isolated gene (AAT29824) obt'd. from a canine liver DNA library. The
cloning of the IgE gene allows prodn. of large quantities of recombinant
IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE
can be used in drug development (e.g. small molecule screening, assay
development and anti-IgE antibody generation). Fragments of IgE can be
used in vaccines or to prevent IgE-mediated hypersensitivity. The new
sequence information permits targeted modulation of IgE-mediated immune
responses
XX
SQ Sequence 426 AA;

Query Match      89.7%; Score 87; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPG 16
Db 146 VDGQKATNIFPYTAPG 161

RESULT 12
ABP96583
ID ABP96583 standard; protein; 426 AA.
XX
SQ Sequence 426 AA;

Query Match      89.7%; Score 87; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPG 16
Db 146 VDGQKATNIFPYTAPG 161

ABP96583;
28-MAY-2003 (first entry)
Dog IgE heavy chain amino acid sequence SEQ ID NO:28.
Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
immune response; major histocompatibility complex; MHC; immunogenic;
antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
dermatological; antiinflammatory; IgE-mediated condition; food allergy;
atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
urticaria hives.
Canis familiaris.
WO2003015716-A2.
27-FEB-2003.
08-AUG-2002; 2002WO-US026986.
13-AUG-2001; 2001US-0312120P.
(IGET-) IGE THERAPEUTICS INC.
Chen SA, Yang Y, Barankiewicz T, Chen Z;
WPI; 2003-268242/26.
Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
against IgE, by identifying peptide eliciting CTL response to IgE
peptides naturally presented by major histocompatibility complex class I
protein.
Example 7; Page 152-154; 187pp; English.
The present invention describes a method (M1) for identifying peptides
that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
E (IgE), comprising providing a test peptide (T) suspected of being able
to bind to major histocompatibility complex (MHC) class I molecule, and
evaluating (T) for ability to elicit in a mammal a CTL response to
naturally processed and presented IgE peptides, where a peptide that
induces such a response is identified. Also described are compositions:
(C1) comprising at least one immunogenic peptide (I) identified by (M1);
(C2) comprising at least one isolated polynucleotide encoding (I); and
(C3) comprising antigen-presenting cells that recognise at least one (I).
Where C1-3 are able to bind to at least one MHC class I molecule and to
elicit in a mammal a CTL response to naturally processed and presented
IgE peptides, C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
vasotropic, dermatological, antiinflammatory and cytostatic activities,
and can be used as inducers of a CTL response against IgE, and in
vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
mammal. C1-3 are useful for modulating an IgE-mediated condition such as
IgE-mediated atopic hypersensitivity condition. IgE-mediated non-atopic
hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
useful for treating atopic hypersensitivity conditions (such as allergic
rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
hives). The present sequence represents an IgE heavy chain amino acid
sequence, which is given in an example from the present invention
XX
SQ Sequence 426 AA;
```

```
RESULT 13
ID ABP96584 standard; protein; 577 AA.
XX AC ABP96584;
XX DT 28-MAY-2003 (first entry)
XX DE Duckbilled platypus IgE heavy chain amino acid sequence SEQ ID NO:29.
XX KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cycostatic;
XX dermatological; antiinflammatory; IgE-mediated condition; food allergy;
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX urticaria hives.
XX OS Ornithorhynchus anatinus.
XX PN WO2003015716-A2.
XX PD 27-FEB-2003.
XX PF 08-AUG-2002; 2002WO-US026986.
XX PR 13-AUG-2001; 2001US-0312120P.
XX PA (IGET-) IGE THERAPEUTICS INC.
XX PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX WPI; 2003-268242/26.
XX PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
XX against IgE, by identifying peptide eliciting CTL response to IgE
XX peptides naturally presented by major histocompatibility complex class I
XX protein.
XX Example 7; Page 154-157; 187pp; English.
XX CC The present invention describes a method (M1) for identifying peptides
XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
XX E (IgE), comprising providing a test peptide (T) suspected of being able
XX to bind to major histocompatibility complex (MHC) class I molecule, and
XX evaluating (T) for ability to elicit in a mammal a CTL response to
XX naturally processed and presented IgE peptides, where a peptide that
XX induces such a response is identified. Also described are compositions:
XX (C1) comprising at least one immunogenic peptide (I) identified by (M1);
XX (C2) comprising at least one isolated polynucleotide encoding (I); and
XX (C3) comprising antigen-presenting cells that recognise at least one (I).
XX Where C1-3 are able to bind to at least one MHC class I molecule and to
XX elicit in a mammal a CTL response to naturally processed and presented
XX IgE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
XX vasotropic, dermatological, antiinflammatory and cytostatic activities,
XX and can be used as inducers of a CTL response against IgE, and in
XX vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
XX mammal. C1-3 are useful for modulating an IgE-mediated condition such as
XX IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
XX hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
XX useful for treating atopic hypersensitivity conditions (such as allergic
XX rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
XX atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
XX hives). The present sequence represents an IgE heavy chain amino acid
XX sequence, which is given in an example from the present invention
XX
XX Sequence 577 AA;
XX
XX Query Match 79.4%; Score 77; DB 6; Length 577;
XX Best Local Similarity 77.8%; Pred. No. 0.0049; Indels 0; Gaps 0;
XX Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
ID AAB06204 standard; protein; 343 AA.
XX AC AAB06204;
XX DT 22-NOV-2000 (first entry)
XX DE Platypus IgE heavy chain constant regions 2, 3 and 4.
XX KW Platypus; immunoglobulin E; IgE; vaccination; infection; allergy; asthma;
XX eczema; immunogenic peptide.
XX OS Ornithorhynchus anatinus.
XX PN WO2000025722-A2.
XX PD 11-MAY-2000.
XX PF 21-OCT-1999; 99WO-SE001896.
XX PR 02-NOV-1998; 98US-0106652P.
XX PR 22-SEP-1999; 99US-00401636.
XX PA (RESI-) RESISTENTIA PHARM AB.
XX PI Hellman LT;
XX WPI; 2000-365342/31.
XX PT Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals.
XX
XX Disclosure; Fig 2; 50pp; English.
XX CC The present sequence is an immunogenic peptide consisting of the heavy
XX chain constant regions 2, 3 and 4 of the platypus IgE. It was used to
XX construct a number of immunogenic peptides which consisted of regions of
XX IgE from different mammals, which appear to cause a stronger polyclonal
XX anti-self IgE response than peptides consisting of the same regions from
XX one mammal. Immunogenic peptides, particularly those consisting of
XX different heavy chain constant regions, can be used for vaccination in
XX humans, against bacterial and viral infections and allergies, such as
XX asthma, fur, pollen and food allergies and eczema
XX
XX Sequence 343 AA;
XX
XX Query Match 74.2%; Score 72; DB 3; Length 343;
XX Best Local Similarity 72.2%; Pred. No. 0.002; Indels 0; Gaps 0;
XX Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 15
ID ADF90022 standard; protein; 337 AA.
XX AC ADF90022;
XX DT 26-FEB-2004 (first entry)
```

```

XX Opossum-rat chimeric IgE polypeptide.
DE
XX IGE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;
KW antiasthmatic; dermatological.
XX Chimeric.
OS Didelphis virginiana.
OS Rattus sp.
XX WO2003096966-A2.
PN
XX
PD 27-NOV-2003.
XX
XX 15-MAY-2003; 2003WO-IB002503.
PF
XX
PR 21-MAY-2002; 2002US-0382552P.
PA (RESI-) RESISTENTIA PHARM AB.
XX Lundgren M, Fuentes A, Magnusson A;
PI WPI; 2004-042496/04.
XX N-PSDB; ADF90020, ADF90021.
DR
XX New host cell comprising a nucleic acid vector comprising a
PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or
PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE
PT polypeptide.
XX
XX Claim 3; SEQ ID NO 3; 23pp; English.
PS
XX The present sequence is the protein sequence ofan opossum CH2-rat CH3-
CC opossum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic
CC acid encoding ORO can be used for recombinant production of this chimeric
CC IGE in host, e.g. CHO, cells. The invention provides methods and
CC materials related to expressing chimeric IgE proteins. Nucleic acid
CC vectors, host cells, and methods for producing chimeric IgE polypeptides
CC are provided. When administered to a mammal, the chimeric polypeptides
CC can reduce the IGE antibody effects of IGE-related diseases such as
CC asthma, allergies and eczema.
XX
XX Sequence 337 AA;
SQ
Query March 61.9%; Score 60; DB 8; Length 337;
Best Local Similarity 61.1%; Pred. No. 0.2;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 VDGQKATNIFPYTAPGKQ 18
Db 56 VDGGQEANLFFYTTPRKR 73

```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 10.7273 Seconds
(without alignments)
161.448 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDGQKATNIPPYTPAGKQ 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.5	270	2 T16880	hypothetical prote
2	43	44.3	633	2 S62057	proline-rich prote
3	43	44.3	658	2 AH0110	probable surface p
4	42	43.3	381	2 AD2436	ATP-binding protei
5	42	43.3	643	1 S15623	E1 protein - human
6	42	43.3	683	2 B71325	conserved hypot het
7	42	43.3	1032	2 S74487	hypothetical prote
8	42	43.3	1686	2 A87692	conserved hypot het
9	41	42.3	241	2 T17798	hypothetical prote
10	41	42.3	544	2 D88449	protein F54D8.3 [1
11	41	42.3	623	2 T22177	hypothetical prote
12	41	42.3	713	2 JE0230	NADPH-cytochrome P
13	41	42.3	2298	2 T49648	hypothetical prote
14	40.5	41.8	363	2 C82607	DNA primase XF2025
15	40.5	41.8	1371	2 D82606	DNA primase XF2061
16	40	41.2	101	2 G69203	conserved hypot het
17	40	41.2	109	2 F89886	hypothetical prote
18	40	41.2	179	2 D90167	conserved hypot het
19	40	41.2	227	2 C75582	conserved hypot het
20	40	41.2	240	2 C89967	serine proteinase
21	40	41.2	242	1 LXB5	licheninase (EC 3.
22	40	41.2	258	2 AF0306	puative trans-acon
23	40	41.2	327	2 S40753	hypothetical prote
24	40	41.2	374	2 G81926	probable polyamine
25	40	41.2	391	2 T32714	hypothetical prote
26	40	41.2	419	2 C81179	spermidine/putresc
27	40	41.2	454	2 AH2821	conserved hypot het
28	40	41.2	470	2 H97599	BH0982 hypot hetica
29	40	41.2	506	2 T07942	probable squalene

30	40	41.2	645	2 T16078	hypothetical prote
31	40	41.2	812	2 T07745	phosphatidylinosit
32	40	41.2	814	2 T07761	phosphatidylinosit
33	40	41.2	831	2 T05265	coat protein gamma
34	40	41.2	857	1 QQB81L	glycoprotein B - h
35	40	41.2	915	2 T12526	hypothetical prote
36	40	41.2	1013	2 G71460	probable outer mem
37	40	41.2	1064	2 T40751	isoleucyl-trna syn
38	40	41.2	1203	2 T28895	hypothetical prote
39	40	41.2	3069	2 H70656	fatty-acid synthas
40	40	41.2	3076	2 A87058	fatty acid synthas
41	39	40.2	157	2 A69637	transcription elon
42	39	40.2	213	2 C64041	hypothetical prote
43	39	40.2	308	2 H95965	hypothetical prote
44	39	40.2	308	2 F95416	hypothetical prote
45	39	40.2	374	2 G86267	T6J4.7 protein - A

ALIGNMENTS

RESULT 1
T16880
hypothetical protein T14G12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-Oct-2004
C;Accession: T16880
R;Wilcox, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid T14G12.
A;Reference number: Z18596
A;Accession: T16880
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-270 <WIL>
A;Cross-references: UNIPROT:Q22510; UNIPARC:UPI00000075025; EMBL:U41268; NID:g1086843; PI
C;Genetics:
A;Gene: CESP:T14G12.4
A;Introns: 37/1; 72/3; 164/1
F;93-185/Domain: fork head DNA-binding domain homology <FHD>

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 3 GQKATNIPPYTPAG 16
Db 205 GAAGANLFFPYFSPG 218

RESULT 2
S62057
proline-rich protein LAS17 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O4724; protein YOR181w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S62057; S67073
R;Toh-e, A.
submitted to the EMBL Data Library, December 1995
A;Description: Yeast mutants sensitive to local anesthetics.
A;Reference number: S62057
A;Accession: S62057
A;Molecule type: DNA
A;Residues: 1-633 <TOH>
A;Cross-references: UNIPROT:Q12446; UNIPARC:UPI0000003CA29; EMBL:D78487; NID:g1101756; PI
R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S67073
A;Molecule type: DNA
A;Residues: 1-633 <HUG>
A;Cross-references: UNIPARC:UPI0000003CA29; EMBL:Z75089; NID:gl420436; PID:e252060; PID:g
A;Experimental source: strain S289C

C;Genetics:

A;Gene: SGD:LAS17
A;Cross-references: SGD:S0005707; MIPS:YOR181w
A;Map position: 15R

Query Match 44.3%; Score 43; DB 2; Length 633;
Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 QKATNIPPYTPAGKQ 18
| ||| ||| : :
Db 283 QSATNPPFPVPQQQ 297

RESULT 3

AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0110
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0110
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-658 <KUR>
A;Cross-references: UNIPROT:Q8ZHU0; UNIPARC:UPI00000CD765; GB:AL590842; PIDN:CAC89747.1;
C;Genetics:
A;Gene: YPO0902

Query Match 44.3%; Score 43; DB 2; Length 658;
Best Local Similarity 61.5%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VDQKATNIPPVT 13
: ||||| :
Db 99 LQGQATNLAPAT 111

RESULT 4

AD2436
ATP-binding protein of polyamine ABC transporter all5044 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004
C;Accession: AD2436
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2436
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <KUR>
A;Cross-references: UNIPROT:Q8VM92; UNIPARC:UPI00000CED3F; GB:BA0000019; PIDN:BAB76743.1;
C;Genetics:
A;Gene: all5044

Query Match 43.3%; Score 42; DB 2; Length 381;
Best Local Similarity 53.3%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDQKATNIPPVTAP 15
: || ||||| :
Db 80 IQGQPMTNIPPYRRP 94

RESULT 5

S15623
E1 protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15623
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M. Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 2b
A;Reference number: S15614; MUID:91188699; PMID:1964523
A;Accession: S15623
A;Molecule type: DNA
A;Residues: 1-643 <HIR>
A;Cross-references: UNIPROT:P22153; UNIPARC:UPI000013813; EMBL:X55965; NID:G60882; PIDN:Q00000
C;Superfamily: papillomavirus E1 protein
C;Keywords: early protein

Query Match 43.3%; Score 42; DB 1; Length 643;
Best Local Similarity 53.8%; Pred. No. 51;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 KATNIPPYTPAGK 17
| ||| ||| : :
Db 581 KFTNPPFPASPG 593

RESULT 6

B71325
conserved hypothetical protein TP0421 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: B71325
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khajak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDougal, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: B71325
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-683 <COL>
A;Cross-references: UNIPROT:Q83436; UNIPARC:UPI00000COA71; GB:AE001220; GB:AE000520; NID:Q00000
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0421

Query Match 43.3%; Score 42; DB 2; Length 683;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIPPYTPAG 16
| ||| : : |||
Db 278 GQKSARFFGFSAPG 291

RESULT 7

S74487
hypothetical protein sl11060 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74487
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC 6803
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74487
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;RESIDUES: 1-713 <IAM>
A;Cross-references: UNIPROT:Q7M275; UNIPARC:UPI0000175049

C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; oxidoreductase
 C;Keywords: Flavoprotein; oxidoreductase
 F;107-712/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F;109-257/Domain: flavodoxin homology <FLX>

Query Match 42.3%; Score 41; DB 2; Length 713;
 Best Local Similarity 57.1%; Pred. No. 85;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQKATNIPFYTA 14
 :||| ||| |||
 Db 265 LGGDTRATPYTA 278

RESULT 13

T49648
 C;Species: Neurospora crassa
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C;Accession: T49648
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
 A;Reference number: Z25022
 A;Accession: T49648
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-2298 <SCH>
 A;Cross-references: UNIPROT:Q96U00; UNIPARC:UPI000017B4BA; EMBL.ALJ55933; GSPDB:GN00116;
 A;Experimental source: BAC clone B8B20; strain OR74A
 C;Genetics:
 A;Gene: NCSP:B8B20.20
 A;Map position: 6
 A;Introns: 426/3

Query Match 42.3%; Score 41; DB 2; Length 2298;
 Best Local Similarity 42.9%; Pred. No. 3.1e+02;
 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 4 QKATNIPFYTAGK 17
 : : ||| |||
 Db 1694 ERVTQVLPYFQPGK 1707

RESULT 14

C82607
 C;Species: Xylella fastidiosa (strain 9a5c)
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: C82607
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: C82607
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-363 <STM>
 A;Cross-references: UNIPROT:Q9P6W0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328

A;Contents: annotation
 C;Genetics:
 A;Gene: XF2025

Query Match 41.8%; Score 40.5; DB 2; Length 363;
 Best Local Similarity 55.6%; Pred. No. 49;
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VDQKATNIPFYTAGKQ 18
 ||| | ||| |||
 Db 284 VDG---TAFPPFAPGGEQ 298

RESULT 15

D82606
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: D82606
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: D82606
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1371 <SIM>
 A;Cross-references: UNIPROT:Q9P6B8; UNIPARC:UPI00000C290E; GB:AE004022; GB:AE003849; NID
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF2061

Query Match 41.8%; Score 40.5; DB 2; Length 1371;
 Best Local Similarity 55.6%; Pred. No. 2.2e+02;
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VDQKATNIPFYTAGKQ 18
 ||| | ||| |||
 Db 1292 VDG---TAFPPFAPGGEQ 1306

Search completed: August 30, 2006, 04:30:56
 Job time : 11:7273 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:22:32 ; Search time 70.1818 Seconds
(without alignments)
237.245 Million cell updates/sec

Title: US-10-758-165a-10

Perfect score: 97

Sequence: 1 VDGQKATNIFPYTAPKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	52.6	382	2	Q7P5V1_FUSNV
2	51	52.6	382	2	Q8R6B3_FUSNN
3	48	49.5	168	2	Q95QA9_CABEL
4	48	49.5	270	2	Q22510_CABEL
5	48	49.5	1143	2	Q3N7V1_9PROT
6	47	48.5	365	2	Q36VF1_RHOPA
7	47	48.5	1054	2	Q608X6_METCA
8	47	48.5	1538	2	Q94H26_ORYSA
9	46	47.4	408	2	Q565U8_9BACT
10	45.5	46.9	491	2	Q2L2W7_BORAV
11	45	46.4	279	2	Q619H6_CAEBR
12	45	46.4	445	1	ALN_STRCO
13	45	46.4	811	2	Q41FN3_GIBZE
14	45	46.4	908	2	Q2ZH01_CALSA
15	44	45.4	102	1	GAGC1_HUMAN
16	44	45.4	102	2	Q61B11_HUMAN
17	44	45.4	340	2	Q9AYA0_ORYSA
18	44	45.4	525	2	Q6ALL1_DESPS
19	44	45.4	589	2	Q53Q04_ORYSA
20	44	45.4	760	2	Q6UUM4_ORYSA
21	44	45.4	875	2	Q7FAL9_ORYSA
22	44	45.4	884	2	Q53JX1_ORYSA
23	44	45.4	1037	2	Q551S1_CRYNE
24	44	45.4	1037	2	Q5KXC8_CRYNE
25	44	45.4	1436	2	Q7FAL2_ORYSA
26	44	45.4	1685	2	Q7XSP1_ORYSA
27	44	45.4	2096	2	Q2R0G5_ORYSA
28	43.5	44.8	398	2	Q413E1_KINRA
29	43.5	44.8	1238	2	Q5FK37_LACAC
30	43	44.3	52	2	Q7WYM4_BACSH
31	43	44.3	104	2	Q5TSY2_ANOGA

32	43	44.3	166	2	Q6GCH5_STAAS	Q6GCH5 staphylococ
33	43	44.3	166	2	Q8NYE3_STAAM	Q8NYE3 staphylococ
34	43	44.3	240	2	Q9KH50_STAAM	Q9KH50 staphylococ
35	43	44.3	240	2	Q2YTM3_STAAB	Q2YTM3 staphylococ
36	43	44.3	240	2	Q5HEW1_STAAB	Q5HEW1 staphylococ
37	43	44.3	240	2	Q6G8C2_STAAS	Q6G8C2 staphylococ
38	43	44.3	240	2	Q8NVX6_STAAM	Q8NVX6 staphylococ
39	43	44.3	294	2	Q36RK4_MARHY	Q36RK4 marionbacte
40	43	44.3	343	1	QUEA_BORBU	Q51053 borrelia bu
41	43	44.3	346	2	Q662Z1_BORGA	Q662Z1 borrelia ga
42	43	44.3	400	2	Q8GGD4_CORST	Q8GGD4 corynebacte
43	43	44.3	633	1	LAS17_YEAST	Q12446 saccharomyc
44	43	44.3	641	2	Q8CKM1_YERPE	Q8CKM1 yersinia pe
45	43	44.3	658	2	Q8ZHJ0_YERPE	Q8ZHJ0 yersinia pe

ALIGNMENTS

RESULT 1

ID Q7P5V1_FUSNV PRELIMINARY; PRT; 382 AA.
AC Q7P5V1;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).
GN Names=FNVI343;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 49256;
RA Karpatrial V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyrpides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AABF01000055; EAA24105.1; -; Genomic_DNA.

DR GO; GO:0016829; F-lyase activity; IEA.

DR InterPro; IPR010327; HGD-D.

DR Pfam; PF06050; HGD-D; 1.

SQ SEQUENCE 382 AA; 43893 MW; 441C73816E1C761E CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;

Best Local Similarity 64.3%; Pred. No. 9.1;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGOKATNIFPYTAP 15

Db 28 EGKKAUGIFFPYAP 41

RESULT 2

ID Q8R6B3_FUSNN PRELIMINARY; PRT; 382 AA.

AC Q8R6B3;

DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2002, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).

GN OrderedLocustNames=FN0208;

OS Fusobacterium nucleatum subsp. nucleatum.

OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;

```
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 25586;
RX MEDLINE=21866394; PubMed=11889109;
RX DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyriades N.C., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE009951; AAL94414.1; -; Genomic_DNA.
DR BioCyc; FNUC190304:FN0208-MONOMER; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR010327; HGD-D.
DR Pfam; PF06050; HGD-D; 1.
DR Complete proteome; Lyase.
KW SEQUENCE 382 AA; 43923 MW; 93038D4296AE34CD CRC64;
SQ
Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 9.1;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DGQKATNIFPYTAP 15
Db 28 EGKKAIGFPPYAP 41
:|||||
-----
RESULT 3
Q95QA9_CABEL
ID Q95QA9_CABEL PRELIMINARY; PRT; 168 AA.
AC Q95QA9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 28.
DE Forkhead transcription factor family protein 2, isoform b.
GN Name=fkh-2; ORFNames=T14G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- INTERACTION:
CC Q9XW88:php-3; NbExp=1; IntAct=EBI-327741, EBI-316766;
CC Q21648:R02F2.5; NbExp=1; IntAct=EBI-327741, EBI-314179;
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; U41268; AAA82436.1; -; Genomic_DNA.
DR PIR; T16880; T16880.
DR HSSP; Q99958; 1DSV.
DR SMR; Q22510; 93-170.
DR IntAct; Q22510; -.
DR WormBase; WBGene00001434; fkh-2.
DR WormPep; T14G12.4a; CE04965.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK HEAD 1; 1.
DR PROSITE; PS00658; FORK HEAD 2; 1.
DR PROSITE; PS00039; FORK HEAD 3; 1.
DR Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 270 AA; 30491 MW; 7C49116E5EC76175 CRC64;
Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00658; FORK HEAD 2; 1.
DR PROSITE; PS00039; FORK HEAD 3; 1.
DR Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 168 AA; 19239 MW; 8E01AC4E69968572 CRC64;
Query Match 49.5%; Score 48; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 3 GQKATNIFPYTAPG 16
Db 103 GAAAANLFPYFSPG 116
|:|:|:|:|
-----
RESULT 4
Q22510_CABEL
ID Q22510_CABEL PRELIMINARY; PRT; 270 AA.
AC Q22510;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 39.
DE Forkhead transcription factor family protein 2, isoform a.
GN Name=fkh-2; ORFNames=T14G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- INTERACTION:
CC Q9XW88:php-3; NbExp=1; IntAct=EBI-327741, EBI-316766;
CC Q21648:R02F2.5; NbExp=1; IntAct=EBI-327741, EBI-314179;
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; U41268; AAA82436.1; -; Genomic_DNA.
DR PIR; T16880; T16880.
DR HSSP; Q99958; 1DSV.
DR SMR; Q22510; 93-170.
DR IntAct; Q22510; -.
DR WormBase; WBGene00001434; fkh-2.
DR WormPep; T14G12.4a; CE04965.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK HEAD 1; 1.
DR PROSITE; PS00658; FORK HEAD 2; 1.
DR PROSITE; PS00039; FORK HEAD 3; 1.
DR Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 270 AA; 30491 MW; 7C49116E5EC76175 CRC64;
Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```

QY      3 GQKATNIFPVTAPG 16
      | | | | | | | | | |
Db     205 GAAANLFPYFSPG 218

RESULT 5
Q3N7V1_9PROT
ID   Q3N7V1_9PROT    PRELIMINARY;   PRT; 1143 AA.
AC   Q3N7V1;
DT   25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Putative type 4 fibrial biogenesis protein Pily1 precursor.
GN   ORFNames=NEUTDRAFT_0559;
OS   Nitrosomonas eutropha C71.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC   Nitrosomonadaceae; Nitrosomonas.
OX   NCBI_TaxID=335283;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C71;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA   Hammon N., Israeli S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Nitrosomonas eutropha
RT   C71.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C71;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA   Hammon N., Israeli S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Nitrosomonas eutropha
RT   C71.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC   -1- CAUTION: The sequence shown here is derived from an
CC   EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC   preliminary data.
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AAJ01000019; EAO16686.1; -; Genomic_DNA.
KW   Signal.
FT   SIGNAL
SQ   SEQUENCE 1143 AA; 123766 MW; 9C270A88F6A0FAF1 CRC64;

Query Match      49.5%; Score 48; DB 2; Length 1143;
Best Local Similarity 64.3%; Pred. No. 95;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 DGOKATNIFPVTAP 15
      | | | | | | | | | |
Db     383 DGSKLTNHFNTSP 396

RESULT 6
Q36VF1_RHOPA
ID   Q36VF1_RHOPA    PRELIMINARY;   PRT; 365 AA.
AC   Q36VF1;
DT   06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT   06-DEC-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=RPEDRAFT_0215;
OS   Rhodopseudomonas palustris BisA53.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Rhodopseudomonas.
OX   NCBI_TaxID=316055;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BisA53;

```

```

RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA   Hammon N., Israeli S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Rhodopseudomonas
RT   palustris BisA53.";
RL   Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BisA53;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome of Rhodopseudomonas palustris
RT   BisA53.";
RL   Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC   -1- CAUTION: The sequence shown here is derived from an
CC   EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC   preliminary data.
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AALA01000029; EAO87857.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE 365 AA; 40239 MW; E11D3C9BC0F1244F CRC64;

Query Match      48.5%; Score 47; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 VDGOKATNIFPVTAPG 16
      | | | | | | | | | |
Db     75 LDGLKAGQVPIYLGPG 90

RESULT 7
Q608X6_METCA
ID   Q608X6_METCA    PRELIMINARY;   PRT; 1054 AA.
AC   Q608X6;
DT   23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT   23-NOV-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Hydrophobe/amphiphile Efflux-1 (HAE1) family protein.
GN   OrderedLocNames=MCA1360;
OS   Methylococcus capsulatus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC   Methylococcaceae; Methylococcus.
OX   NCBI_TaxID=414;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bath / NCIMB 11132;
RX   PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
RA   Ward N.L., Larsen O., Sakwa J., Bruseth L., Khouri H.M., Durkin A.S.,
RA   Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
RA   Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,
RA   Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,
RA   Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
RA   Grindhaug S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S.,
RA   Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,
RA   Eisen J.A.;
RT   "Genomic insights into methanotrophy: the complete genome sequence of
RT   Methylococcus capsulatus (Bath).";
RL   PLoS Biol. 2:1616-1628(2004).
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AE017282; AAU92574.1; -; Genomic_DNA.
DR   TIGR; MCA1360; -
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR001036; Acrflavin_res.
DR   InterPro; IPR004764; HAE1.

```

```

DR Pfam; PF00873; ACR tran; 1.
DR PRINTS; PR00702; ACRIFAVINRP.
DR TIGRFAMs; TIGR00915; 2A0602; 1.
KW Complete proteome.
SQ SEQUENCE 1054 AA; 115005 MW; BB032CB91B38D1A8 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1054;
Best Local Similarity 56.2%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQKATNIFPYTAPG 16
Db 294 VNGHKSTQIVVYTLPG 309

RESULT 8
Q94H26 ORYSA PRELIMINARY; PRT; 1538 AA.
AC Q94H26;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 18.
DE Putative gag-pol polyprotein.
GN Name=OSJNB0077G22.13;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNB0077G22 genomic sequence.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AC084831; AAK52152.1; -; Genomic_DNA.
DR Gramene; Q94H26; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0015074; P:DNA integration; IEA.
DR InterPro; IPR005162; Retrotrans gag.
DR InterPro; IPR008916; Retrov capsid_C.
DR InterPro; IPR002156; RNase_H.
DR InterPro; IPR001584; Rve.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF06665; rve; 1.
DR PROSITE; PS00994; INTEGRASE; 1.
DR PROSITE; PS00879; RNASE_H; 1.
KW Polyprotein.
SQ SEQUENCE 1538 AA; 174629 MW; 5E7A521B398BC776 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1538;
Best Local Similarity 61.5%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDQKATNIFPYT 13
Db 740 VDGRAAVNLMPYT 752

RESULT 9

```

```

Q565U8_9BACT PRELIMINARY; PRT; 408 AA.
AC Q565U8;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DE 3-oxoacyl-CoA thiolase.
GN ORFNames=fc62;
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15997700; DOI=10.1016/j.syapm.2005.02.006;
RA Kube M., Beck A., Meyerdiets A., Amann R., Reinhardt R., Rabus R.;
RT "A catabolic gene cluster for anaerobic benzoate degradation in
RT methanotrophic microbial Black Sea mats.";
RL Syst. Appl. Microbiol. 28:287-294(2005).
CC -|- SIMILARITY: Belongs to the thiolase family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; CR931837; CAI78864.1; -; Genomic_DNA.
DR InterPro; IPR002155; Thiolase.
DR PANTHER; PTHR18919; Thiolase; 2.
DR Pfam; PF02803; Thiolase_C; 1.
DR Pfam; PF00108; Thiolase_N; 1.
DR TIGRFAMs; TIGR01930; ACCoA-C-Actrans; 1.
DR PROSITE; PS00737; THIOLEASE 2; 1.
SQ SEQUENCE 408 AA; 43389 MW; F9BEC546AF32193 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 408;
Best Local Similarity 38.9%; Pred. No. 70;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VDQKATNIFPYTAPGKQ 18
Db 45 IDASIGANVIQFTAPGAQ 62

RESULT 10
Q2L2W7 BORAV PRELIMINARY; PRT; 491 AA.
AC Q2L2W7;
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DT 07-MAR-2006, entry version 1.
DE Putative phage portal protein.
GN ORFNames=BAV1315; 197N.
OS Bordetella avium 197N.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=360910;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=197N;
RA Sebaihia M.;
RT "The genome sequence of the poultry pathogen Bordetella avium, and
RT genomic comparisons with related species infecting mammals.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AM167904; CAJ48922.1; -; Genomic DNA.
SQ SEQUENCE 491 AA; 54500 MW; E900B690162C1AA4 CRC64;

Query Match 46.9%; Score 45.5; DB 2; Length 491;
Best Local Similarity 47.6%; Pred. No. 1e+02;
Matches 10; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

Qy 3 GQKATNIF-----PYTAPG 16

```



```
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhalil B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Fato S., Ferreira P., FitzGerald M., Gage D.,
RA Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,
RA Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamat M., Karmali A.,
RA Karatas A., Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrum J.,
RA Meneses L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
RA Purcell S., Rachupka A., Ramsamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schupback R., Seaman S., Severy P.,
RA Smirnov S., Smith C., Spencer B., Stangor-Thomann N., Stojanovic N.,
RA Stubbs M., Talamas J., Testave S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AACW01000168; EAA73443.1; -; Genomic_DNA.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR001461; Peptidase_A1.
DR PANTHER; PTHR13683; Peptidase_A1; 1.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 811 AA; 84248 MW; C3C54A02E10DA79 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 811;
Best Local Similarity 58.8%; Pred.No. 2.1e+02;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 DGQKATNIFPYTPAGKQ 18
DB 676 DDDKETATGGYTPAGKQ 692

RESULT 14
Q2ZH01 CALSA
ID Q2ZH01 CALSA PRELIMINARY; PRT; 908 AA.
AC Q2ZH01
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Conserved membrane protein.
DE ORFNames=CgscDRAFT_0884;
OS Caldicellulosiruptor saccharolyticus DSM 8903.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
OC Caldicellulosiruptor.
OX NCBI_TaxID=351627;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 8903;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Caldicellulosiruptor
saccharolyticus DSM 8903.";
```

```
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 8903;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Caldicellulosiruptor
saccharolyticus DSM 8903.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AALW01000031; EAP42636.1; -; Genomic_DNA.
DR SEQUENCE 908 AA; 105151 MW; B5E42A7161E5ED12 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 908;
Best Local Similarity 38.9%; Pred.No. 2.4e+02;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTPAGKQ 18
DB 576 LDGYTKNYYPYSEPTEE 593

RESULT 15
GAGC1 HUMAN
ID GAGC1 HUMAN STANDARD; PRT; 102 AA.
AC O60823;
DT 11-JAN-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 36.
DE G antigen family C 1 protein (Prostate-associated gene 4 protein)
DE (PAGE-4) (PAGE-1) (GAGE-9).
GN Name=PAGE4; Synonyms=GAGEC1; ORFNames=JM27;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA]
RX MEDLINE=98393718; PubMed=9724777; DOI=10.1073/pnas.95.18.10757;
RA Brinkmann U., Vasmatazis G., Lee B., Yerushalmi N., Essand M.,
RA Pastan I.;
RT "PAGE-1, an X chromosome-linked GAGE-like gene that is expressed in
normal and neoplastic prostate, testis, and uterus.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10757-10762(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC Strom T.M., Nyakatura G., Hellebrand H., Drescher B., Rosenthal A.,
RA Meindl A.;
RT "Transcription map in Xp11.23.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15772651; DOI=10.1038/nature03440;
RA Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,
RA Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
RA Jones M.C., Hurler M.E., Andrews T.D., Scott C.E., Searle S., Chen R.,
RA Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,
RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Aradhya S.,
RA Ashwell R.I., Babbage A.K., Baggeley C.L., Ballabio A., Banerjee R.,
RA Barker G.B., Barlow K.F., Barrett I.P., Bates K.N., Beards D.M.,
RA Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
```

RA Bruford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,
RA Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
RA Chavez D., Chen E., Chen G., Chen Y., Chen Z., Chinault C.,
RA Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
RA Dalgado O., Deshazo D., Dhama P., Ding Y., Dinh H., Dodsworth S.,
RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
RA Bades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
RA Faulkner L., Francis F., Frankland J., Fraser A.E., Gaiagoczy P.,
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
RA Hawes A., Heath P.D., Heilmann K., Hennig S., Hernandez J.,
RA Hinzmann B., Ho S., Hoffs M., Howden P.J., Huckle E.J., Hume J.,
RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
RA De Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA Kioschis P., Klages S., Knights A.J., Koslura A., Kovar-Smith C.,
RA Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
RA Lloyd C., Lloyd D.M., Loulsegod H., Loveland J.E., Lovell J.D.,
RA Lozado R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
RA McDowell J., McLaren S., McMurray A., Meidl P., Meitinger T.,
RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA Mullikin J.C., Nguyen N., Nordsiek G., Nyakatura G., O'dell C.N.,
RA Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA Ridler K.A., Schlesinger D., Schueler M.G., Sehra H.K.,
RA Shaw-Smith C., Shen H., Sheridan E.M., Showkneen R., Skuce C.D.,
RA Smith M.L., Soheran E.C., Steingruber H.E., Steward C.A., Storey R.,
RA Swann R.M., Swarbrick D., Tabor P.E., Taudien S., Taylor T.,
RA Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
RA Tromans A.C., d'Urso M., Verdusco D., Villasana D., Waldron L.,
RA Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,
RA Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
RA Williams G., Williams L., Williamson A., Williamson H., Wilming L.,
RA Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
RA Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,
RA Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
RA Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,
RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
RT "The DNA sequence of the human X chromosome."
RL Nature 434:325-337(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Unknown.
CC -!- TISSUE SPECIFICITY: Preferentially expressed in normal male and
CC female reproductive tissues, prostate, testis, fallopian tube,
CC uterus, and placenta, as well as in prostate cancer, testicular
CC cancer, and uterine cancer.
CC -!- SIMILARITY: Belongs to the GAGE family.

CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AF275258; AAF88037.1; -; mRNA.
DR EMBL: AJ005894; CAA06751.1; -; mRNA.
DR EMBL: AP238380; -; NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL: BC010897; AAH10897.1; -; mRNA.
DR Ensembl: ENSG00000101951; Homo sapiens.
DR H-InvDB: HIX0016804; -;
DR HGNC: HGNC:4108; PAGE4.
DR MIM: 300287; Gene.
DR LinkHub: O60829; -;
DR InterPro: IPR008625; GAGE.
DR PANTHER: PTHR14047; GAGE; 1.
DR Pfam: PF05831; GAGE; 1.
FT CHAIN 1 102 G antigen family C 1 protein.
FT /FTId=PRO_0000148348.
SQ SEQUENCE 102 AA; 11153 MW; CE5D07AFBF73301B CRC64;
Query Match 45.4%; Score 44; DB 1; Length 102;
Best Local Similarity 43.8%; Pred. No. 35;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 2 DGQKATNIPPYTAPGX 17
DB 14 DGQEAPEVDVAFVAPGE 29
||||| : : |||:
Search completed: August 30, 2006, 04:29:18
Job time : 72.1818 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 17.8182 Seconds
(without alignments)
88.424 Million cell updates/sec

Title: US-10-758-165a-10

Perfect score: 97

Sequence: 1 VDGQKATNIPFYTAGKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	97	100.0	431	2	US-09-479-614-14
2	97	100.0	496	2	US-09-479-614-2
3	97	100.0	496	2	US-09-479-614-29
4	87	89.7	108	2	US-09-281-760E-35
5	87	89.7	312	2	US-09-701-623C-2
6	87	89.7	426	1	US-08-336-583-2
7	87	89.7	426	5	PCT-US95-13795-2
8	77	79.4	343	2	US-09-401-636-7
9	60	61.9	341	2	US-09-401-636-3
10	60	61.9	341	2	US-09-401-636-4
11	60	61.9	341	2	US-09-401-636-6
12	60	61.9	341	2	US-09-401-636-9
13	60	61.9	341	2	US-09-401-636-11
14	60	61.9	342	2	US-09-401-636-5
15	60	61.9	342	2	US-09-401-636-8
16	60	61.9	345	2	US-09-401-636-10
17	42	43.3	449	2	US-09-252-991A-28547
18	42	43.3	985	2	US-09-993-777-6
19	42	43.3	985	2	US-09-993-777-66
20	42	43.3	985	2	US-09-994-064-20
21	42	43.3	985	2	US-09-994-064-66
22	42	43.3	985	5	PCT-US96-03916-6
23	42	43.3	985	5	PCT-US96-03916-66
24	41	42.3	135	2	US-09-252-991A-30004
25	41	42.3	232	2	US-09-489-039A-8106
26	41	42.3	497	2	US-10-077-699C-5

27 40 41.2 63 2 US-09-612-402B-29 Sequence 29, Appl
28 40 41.2 63 2 US-09-542-520-29 Sequence 29, Appl
29 40 41.2 242 2 US-09-286-690-8 Sequence 8, Appl
30 40 41.2 391 2 US-09-721-870-38 Sequence 38, Appl
31 40 41.2 503 2 US-09-147-009-11 Sequence 11, Appl
32 40 41.2 505 2 US-09-612-402B-17 Sequence 17, Appl
33 40 41.2 505 2 US-09-542-520-17 Sequence 17, Appl
34 40 41.2 659 2 US-09-248-796A-24809 Sequence 24809, A
35 40 41.2 670 2 US-10-197-220-169 Sequence 169, App
36 40 41.2 829 2 US-10-055-364-46 Sequence 46, Appl
37 40 41.2 854 2 US-09-350-841A-1589 Sequence 1589, Ap
38 40 41.2 856 2 US-08-486-099-103 Sequence 103, App
39 40 41.2 856 2 US-08-484-223B-103 Sequence 103, App
40 40 41.2 856 2 US-08-919-597-103 Sequence 103, App
41 40 41.2 856 2 US-08-475-668A-103 Sequence 103, App
42 40 41.2 856 2 US-08-485-551A-103 Sequence 103, App
43 40 41.2 856 2 US-08-471-913A-103 Sequence 103, App
44 40 41.2 856 2 US-08-485-264A-103 Sequence 103, App
45 40 41.2 856 2 US-08-474-349A-103 Sequence 103, App

ALIGNMENTS

RESULT 1

US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 100.0%; Score 97; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGKQ 18
| | | | | | | | | | | | | | | | | | | | | |
Db 151 VDGQKATNIPFYTAGKQ 168

RESULT 2

US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

US-09-479-614-2

Query Match 100.0%; Score 97; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGKQ 18
 |||||
 Db 216 VDGQKATNIPFYTAGKQ 233

RESULT 3

US-09-479-614-29
 ; Sequence 29, Application US/09479614
 ; Patent No. 6573372
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catharine
 ; APPLICANT: Weber, Eric
 ; TITLE OF INVENTION: Peline Immunoglobulin E Molecules and Related Methods
 ; FILE REFERENCE: P-1047
 ; CURRENT APPLICATION NUMBER: US/09/479,614
 ; CURRENT FILING DATE: 2000-01-07
 ; EARLIER APPLICATION NUMBER: 60/115,033
 ; EARLIER FILING DATE: 1999-01-07
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 29
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Felis catus
 US-09-479-614-29

Query Match 100.0%; Score 97; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGKQ 18
 |||||
 Db 216 VDGQKATNIPFYTAGKQ 233

RESULT 4

US-09-281-760E-35
 ; Sequence 35, Application US/09281760E
 ; Patent No. 6734287
 ; GENERAL INFORMATION:
 ; APPLICANT: Lawton, Robert
 ; APPLICANT: Mermer, Brian
 ; APPLICANT: Francoeur, Greg
 ; TITLE OF INVENTION: Specific Binding Protein for Treating
 ; TITLE OF INVENTION: Canine Allergy
 ; FILE REFERENCE: 01-1275A
 ; CURRENT APPLICATION NUMBER: US/09/281,760E
 ; CURRENT FILING DATE: 1999-03-30
 ; PRIOR APPLICATION NUMBER: 09/058,331
 ; PRIOR FILING DATE: 1998-04-09
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 35
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Canis familiaris
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (81)..(81)
 ; OTHER INFORMATION: The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly,
 ; OTHER INFORMATION: Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (82)..(82)
 ; OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.
 ; FEATURE:
 ; NAME/KEY: misc_feature

; LOCATION: (136)..(136)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (413)..(414)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (451)..(451)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (460)..(462)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (500)..(500)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (530)..(530)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (568)..(568)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (847)..(849)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (853)..(853)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1382)..(1382)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1832)..(1832)
 ; OTHER INFORMATION: "n" stands for any nucleic acid
 US-09-281-760E-35

Query Match 89.7%; Score 87; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 8.8e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTAGP 16
 |||||
 Db 47 VDGQKATNIPFYTAGP 62

RESULT 5

US-09-701-623C-2
 ; Sequence 2, Application US/09701623C
 ; Patent No. 681782
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang Ph.D., Chang Yi
 ; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
 ; TITLE OF INVENTION: ALLERGY
 ; FILE REFERENCE: 11514153U1
 ; CURRENT APPLICATION NUMBER: US/09/701,623C
 ; CURRENT FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: PCT/US99/13959
 ; PRIOR FILING DATE: 1999-06-21
 ; PRIOR APPLICATION NUMBER: 09/100,287
 ; PRIOR FILING DATE: 1998-06-20
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 312
 ; TYPE: PRT

```
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2

Query Match      89.7%; Score 87; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      48 VDGQKATNIPFYTAGP 63

RESULT 6
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5628415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2

Query Match      89.7%; Score 87; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      146 VDGQKATNIPFYTAGP 161

RESULT 7
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
```

```
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match      89.7%; Score 87; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      146 VDGQKATNIPFYTAGP 161

RESULT 8
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-7

Query Match      79.4%; Score 77; DB 2; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00013;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGPKQ 18
```

```
Db      61 VDGQAEENLFPYTPAPKR 78
      ||||| |:||||| |:
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPRPKR 79

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPRPKR 79

RESULT 13
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPRPKR 79

RESULT 9
US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPRPKR 79

RESULT 10
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match      61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| |:||||| |:
Db      62 VDGQAEENLFPYTPRPKR 79

RESULT 11
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
```

Search completed: August 30, 2006, 04:33:02
Job time : 17.8182 secs

; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match 61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTPGKQ 18
| | | | | : | | | | | :
Db 62 VDGQEAENLFFYTRPKR 79

RESULT 14
US-09-401-636-5
; Sequence 5, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-5

Query Match 61.9%; Score 60; DB 2; Length 342;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTPGKQ 18
| | | | | : | | | | | :
Db 62 VDGQEAENLFFYTRPKR 79

RESULT 15
US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match 61.9%; Score 60; DB 2; Length 342;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTPGKQ 18
| | | | | : | | | | | :
Db 62 VDGQEAENLFFYTRPKR 79

This Page Blank (uspto)

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 90.9091 Seconds
 (without alignments)
 91.717 Million cell updates/sec

Title: US-10-758-165A-10
 Perfect score: 97
 Sequence: 1 VDGOKATNIPFYTAGKQ 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US07_PUBCOMB.pap.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pap.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10A_PUBCOMB.pap.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pap.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-10
2	97	100.0	431	3	US-09-479-614-14
3	97	100.0	431	4	US-10-409-772-14
4	97	100.0	496	3	US-09-479-614-2
5	97	100.0	496	3	US-09-479-614-29
6	97	100.0	496	4	US-10-214-524-25
7	97	100.0	496	4	US-10-409-772-2
8	97	100.0	496	4	US-10-409-772-29
9	87	89.7	18	5	US-10-758-165-9
10	87	89.7	312	5	US-10-723-207-2
11	87	89.7	426	4	US-10-214-524-28
12	77	79.4	343	3	US-09-401-636-7
13	77	79.4	343	4	US-10-176-664-7
14	77	79.4	343	4	US-10-673-594-7
15	77	79.4	577	4	US-10-214-524-29
16	60	61.9	337	4	US-10-438-794-3
17	60	61.9	337	4	US-10-453-915-3
18	60	61.9	338	4	US-10-438-794-6
19	60	61.9	338	4	US-10-453-915-6
20	60	61.9	341	3	US-09-401-636-3
21	60	61.9	341	3	US-09-401-636-4
22	60	61.9	341	3	US-09-401-636-6
23	60	61.9	341	3	US-09-401-636-9
24	60	61.9	341	3	US-09-401-636-11
25	60	61.9	341	4	US-10-176-664-3
26	60	61.9	341	4	US-10-176-664-4
27	60	61.9	341	4	US-10-176-664-6

Sequence 9, Appli
 Sequence 11, Appli
 Sequence 3, Appli
 Sequence 4, Appli
 Sequence 6, Appli
 Sequence 9, Appli
 Sequence 11, Appli
 Sequence 5, Appli
 Sequence 8, Appli
 Sequence 5, Appli
 Sequence 8, Appli
 Sequence 10, Appli
 Sequence 10, Appli
 Sequence 14, Appli
 Sequence 14, Appli

28 60 61.9 341 4 US-10-176-664-9
 29 60 61.9 341 4 US-10-176-664-11
 30 60 61.9 341 4 US-10-673-594-3
 31 60 61.9 341 4 US-10-673-594-4
 32 60 61.9 341 4 US-10-673-594-6
 33 60 61.9 341 4 US-10-673-594-9
 34 60 61.9 341 4 US-10-673-594-11
 35 60 61.9 342 3 US-09-401-636-5
 36 60 61.9 342 3 US-09-401-636-8
 37 60 61.9 342 4 US-10-176-664-5
 38 60 61.9 342 4 US-10-176-664-8
 39 60 61.9 342 4 US-10-673-594-5
 40 60 61.9 342 4 US-10-673-594-8
 41 60 61.9 345 3 US-09-401-636-10
 42 60 61.9 345 4 US-10-176-664-10
 43 60 61.9 345 4 US-10-673-594-10
 44 60 61.9 347 4 US-10-438-794-14
 45 60 61.9 347 4 US-10-453-915-14

ALIGNMENTS

RESULT 1

US-10-758-165-10
 ; Sequence 10, Application US/10758165
 ; Publication No. US20050196816A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hammerberg, Bruce
 ; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
 ; FILE REFERENCE: 5051-661
 ; CURRENT APPLICATION NUMBER: US/10/758,165
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: US 60/440,472
 ; PRIOR FILING DATE: 2003-01-16
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 10
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Felis catus
 ; ORGANISM: Felis catus
 US-10-758-165-10

Query Match 100.0%; Score 97; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.2e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIPFYTAGKQ 18
 |||||
 Db 1 VDGOKATNIPFYTAGKQ 18

RESULT 2

US-09-479-614-14
 ; Sequence 14, Application US/09479614
 ; Publication No. US20030013183A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine
 ; APPLICANT: Weber, Eric
 ; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 ; FILE REFERENCE: P-1047
 ; CURRENT APPLICATION NUMBER: US/09/479,614
 ; CURRENT FILING DATE: 2000-01-07
 ; EARLIER APPLICATION NUMBER: 60/115,033
 ; EARLIER FILING DATE: 1999-01-07
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Felis catus
 ; ORGANISM: Felis catus
 US-09-479-614-14

```
Query Match      100.0%; Score 97; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      151 VDGQKATNIPFYTAGKQ 168

RESULT 3
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; EARLIER APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match      100.0%; Score 97; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      151 VDGQKATNIPFYTAGKQ 168

RESULT 4
US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match      100.0%; Score 97; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 5
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
```

```
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match      100.0%; Score 97; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 6
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match      100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 7
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2
Query Match      100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 8
US-10-409-772-29
; Sequence 29, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29

Query Match      100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGKQ 18
Db      216 VDGQKATNIPFYTAGKQ 233

RESULT 9
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match      89.7%; Score 87; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGK 16
Db      1 VDGQKATNIPFYTAGK 16
```

```
RESULT 10
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2

Query Match      89.7%; Score 87; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      48 VDGQKATNIPFYTAGP 63

RESULT 11
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match      89.7%; Score 87; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGP 16
Db      1 VDGQKATNIPFYTAGP 16
```

```
Db      146 VDGQKATNIPFYTPAGK 161

RESULT 12
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-7

Query Match      79.4%; Score 77; DB 3; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| :||||| :
Db      61 VDGQKAENLFPYTAPPKR 78

RESULT 13
US-10-176-664-7
; Sequence 7, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7

Query Match      79.4%; Score 77; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| :||||| :
Db      61 VDGQKAENLFPYTAPPKR 78

RESULT 14
US-10-673-594-7
; Sequence 7, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
```

```
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7

Query Match      79.4%; Score 77; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| :||||| :
Db      61 VDGQKAENLFPYTAPPKR 78

RESULT 15
US-10-214-524-29
; Sequence 29, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: ICE-00101.P.1-1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Duckbilled platypus (Ornithorhynchus anatinus)
US-10-214-524-29

Query Match      79.4%; Score 77; DB 4; Length 577;
Best Local Similarity 77.8%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VDGQKATNIPFYTPAGKQ 18
      ||||| :||||| :
Db      295 VDGQKAENLFPYTAPPKR 312

Search completed: August 30, 2006, 05:13:01
Job time : 90.9091 secs
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 9.27273 Seconds
(without alignments)
133.695 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97
Sequence: 1 VDGQKATNIPYTPAGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US09_NEW_PUB.pbp.*
- 2: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	44.3	254	6	US-10-471-571A-726
2	42	43.3	644	7	US-11-330-403-6482
3	42	43.3	644	7	US-11-330-403-15095
4	42	43.3	697	6	US-10-449-902-38427
5	42	43.3	985	7	US-11-342-171-6
6	42	43.3	985	7	US-11-342-171-66
7	41.5	42.8	582	7	US-11-330-403-14312
8	41.5	42.8	582	7	US-11-330-403-15230
9	40.5	41.8	582	7	US-11-330-403-15597
10	39	40.2	361	6	US-10-953-349-19539
11	39	40.2	361	6	US-11-056-3558-59400
12	39	40.2	371	6	US-10-953-349-5963
13	39	40.2	372	6	US-10-953-349-5962
14	39	40.2	374	6	US-10-953-349-5961
15	39	40.2	404	6	US-10-953-349-19538
16	39	40.2	404	6	US-11-056-3558-59399
17	39	40.2	408	6	US-10-953-349-19537
18	39	40.2	408	7	US-11-056-3558-59398
19	39	40.2	467	7	US-11-330-403-1235
20	39	40.2	505	7	US-11-330-403-1258
21	39	40.2	520	7	US-11-330-403-1582
22	39	40.2	520	7	US-11-330-403-11857
23	39	40.2	651	7	US-11-330-403-8900
24	38.5	39.7	394	6	US-10-471-571A-2218
25	38	39.2	55	7	US-11-056-3558-529

26	38	39.2	80	7	US-11-330-403-2450	Sequence 2450, Ap
27	38	39.2	113	6	US-10-471-571A-1112	Sequence 1112, Ap
28	38	39.2	133	7	US-11-056-3558-19986	Sequence 19986, A
29	38	39.2	171	6	US-10-471-571A-2022	Sequence 2022, Ap
30	38	39.2	239	7	US-11-330-403-3689	Sequence 3689, Ap
31	38	39.2	241	6	US-10-471-571A-728	Sequence 728, App
32	38	39.2	250	7	US-11-330-403-15600	Sequence 15600, A
33	38	39.2	287	7	US-11-330-403-1378	Sequence 1378, A
34	38	39.2	328	7	US-11-056-3558-82642	Sequence 82642, A
35	38	39.2	417	7	US-11-056-3558-82642	Sequence 14, Appl
36	38	39.2	502	6	US-10-565-233-14	Sequence 12046, A
37	38	39.2	538	7	US-11-330-403-12046	Sequence 2402, Ap
38	38	39.2	579	7	US-11-330-403-2402	Sequence 6386, Ap
39	38	39.2	579	7	US-11-330-403-6386	Sequence 11265, A
40	38	39.2	579	7	US-11-330-403-11265	Sequence 18232, A
41	38	39.2	581	7	US-11-330-403-1293	Sequence 1293, Ap
42	38	39.2	946	6	US-10-449-902-50315	Sequence 50315, A
43	38	39.2	1070	7	US-10-456-3558-44839	Sequence 44839, A
44	38	39.2	1070	7	US-11-056-3558-46211	Sequence 46211, A
45	38	39.2	1070	7	US-11-056-3558-46211	Sequence 46211, A

ALIGNMENTS

RESULT 1
US-10-471-571A-726
; Sequence 726, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471.571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 726
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(254)
; OTHER INFORMATION: serine protease
US-10-471-571A-726

Query Match 44.3%; Score 43; DB 6; Length 254;
Best Local Similarity 88.9%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 KATNIPPYT 13
Db 58 KDTNIPPYT 66

RESULT 2
US-11-330-403-6482
; Sequence 6482, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330.403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 6482
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Xanthomonas axonopodis pv. glycines

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.25
CURRENT APPLICATION DATA:
APPLICANT: Abad, Mark S.
APPLICATION NUMBER: US/11/342,171
FILING DATE: 27-JAN-2006
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,190
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-11-342-171-66

Query Match 43.3%; Score 42; DB 7; Length 985;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIFPYTAPG 16
| : : : : :
Db 416 GSENTLFPYTPAG 429

RESULT 7
US-11-330-403-14312
; Sequence 14312, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 14312
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Populus tomentosa
US-11-330-403-14312

Query Match 42.8%; Score 41.5; DB 7; Length 582;
Best Local Similarity 57.9%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 VDGQKATNIFPYTA---PG 16
| | | | |
Db 110 VDGSKATGAFILTASHNPG 128

RESULT 8
US-11-330-403-15230
; Sequence 15230, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B

; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15230
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Populus tremula x Populus tremuloides
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(582)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-15230

Query Match 42.8%; Score 41.5; DB 7; Length 582;
Best Local Similarity 57.9%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 VDGQKATNIFPYTA---PG 16
| | | | |
Db 110 VDGSKATGAFILTASHNPG 128

RESULT 9
US-11-330-403-15597
; Sequence 15597, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15597
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Pisum sativum
US-11-330-403-15597

Query Match 41.8%; Score 40.5; DB 7; Length 582;
Best Local Similarity 57.9%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 VDGQKATNIFPYTA---PG 16
| | | | |
Db 110 VDGSKATGAFILTASHNPG 128

RESULT 10
US-10-953-349-19539
; Sequence 19539, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 19539
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19539

Query Match 40.2%; Score 39; DB 6; Length 361;
Best Local Similarity 44.4%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPGKQ 18
| | | | |

Db 124 VDGKKVKRKHPTTEKE 141

RESULT 11

US-11-056-355B-59400

; Sequence 59400, Application US/11056355B

; Publication No. US20060150283A1

; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav

; APPLICANT: Alexandrov, Nikolai

; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

; TITLE OF INVENTION: Polypeptides Encoded Thereby

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/11/056,355B

; CURRENT FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544,190

; PRIOR FILING DATE: 2004-02-13

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 59400

; LENGTH: 361

; TYPE: prt

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: peptide

; LOCATION: (1)...(361)

; OTHER INFORMATION: Ceres Seq. ID no. 14307779

US-11-056-355B-59400

Query Match 40.2%; Score 39; DB 7; Length 361;

Best Local Similarity 44.4%; Pred. No. 65;

Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFPYAPGKQ 18

|||:| | | | |

Db 124 VDGKKVKRKHPTTEKE 141

RESULT 12

US-10-953-349-5963

; Sequence 5963, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 5963

; LENGTH: 371

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-5963

Query Match 40.2%; Score 39; DB 6; Length 371;

Best Local Similarity 54.5%; Pred. No. 66;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GQKATNIPFPYT 13

|:| | | | |

Db 349 GEKIVNLIPYT 359

RESULT 13

US-10-953-349-5962

; Sequence 5962, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

Qy 1 VDGQKATNIPFPYAPGKQ 18

|||:| | | | |

Db 350 GEKIVNLIPYT 360

RESULT 14

US-10-953-349-5961

; Sequence 5961, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 5961

; LENGTH: 374

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-5961

Query Match 40.2%; Score 39; DB 6; Length 374;

Best Local Similarity 54.5%; Pred. No. 67;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GQKATNIPFPYT 13

|:| | | | |

Db 352 GEKIVNLIPYT 362

RESULT 15

US-10-953-349-19538

; Sequence 19538, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 19538

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Glycine max

US-10-953-349-19538

Query Match 40.2%; Score 39; DB 6; Length 404;

Best Local Similarity 44.4%; Pred. No. 73;

Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFPYAPGKQ 18

|||:| | | | |

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 5962

; LENGTH: 372

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-5962

Query Match 40.2%; Score 39; DB 6; Length 372;

Best Local Similarity 54.5%; Pred. No. 67;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GQKATNIPFPYT 13

|:| | | | |

Db 350 GEKIVNLIPYT 360

RESULT 14

US-10-953-349-5961

; Sequence 5961, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 5961

; LENGTH: 374

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-5961

Query Match 40.2%; Score 39; DB 6; Length 374;

Best Local Similarity 54.5%; Pred. No. 67;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GQKATNIPFPYT 13

|:| | | | |

Db 352 GEKIVNLIPYT 362

RESULT 15

US-10-953-349-19538

; Sequence 19538, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 19538

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Glycine max

US-10-953-349-19538

Query Match 40.2%; Score 39; DB 6; Length 404;

Best Local Similarity 44.4%; Pred. No. 73;

Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFPYAPGKQ 18

|||:| | | | |

Db 167 VDGKKVRRKHPYTEKEKE 184

Search completed: August 30, 2006, 04:35:58
Job time : 10.2727 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:29:42 ; Search time 10.7273 Seconds
(without alignments)
161.448 Million cell updates/sec

Title: US-10-758-165a-11
Perfect score: 96
Sequence: 1 IDQKVEQFPQHGVLVKQ 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	51.0	616	2 E85508	hypothetical prote
2	49	51.0	616	2 E90657	hypothetical prote
3	47	49.0	721	2 JC7557	lipidosin - mouse
4	46	47.9	262	2 AG3034	inositol monophosp
5	46	47.9	297	2 E98251	similar to mcbi177
6	45	46.9	1536	1 R8BY53	regulatory protein
7	43	44.8	105	2 T42322	hypothetical prote
8	43	44.8	284	2 G83358	probable ATP-bindi
9	43	44.8	654	2 H86717	hypothetical prote
10	42	43.8	185	2 D95115	thioredoxin family
11	42	43.8	191	2 H97984	conserved hypothet
12	42	43.8	218	2 S76407	phosphoribosylanth
13	42	43.8	271	2 T21777	hypothetical prote
14	42	43.8	359	2 T06532	pyruvate dehydroge
15	42	43.8	359	2 S35157	Delta6 fatty acid
16	42	43.8	702	2 E69498	hypothetical prote
17	42	43.8	817	2 T16409	hypothetical prote
18	42	43.8	1744	2 A54970	tensin, cardiac mu
19	41	42.7	133	2 H72459	probable ribosomal
20	41	42.7	287	1 S76736	hypothetical prote
21	41	42.7	305	2 F86744	tagatose-6-phospha
22	41	42.7	419	2 G84503	hypothetical prote
23	41	42.7	477	2 T37791	probable rna polym
24	41	42.7	535	2 T07969	probable reticulim
25	41	42.7	630	2 T31798	hypothetical prote
26	41	42.7	1020	2 AB0701	tetrathionate redu
27	41	42.7	1270	2 A96669	protein FlN19.11 [
28	41	42.7	2126	2 E70522	probable polyketic
29	40.5	42.2	237	2 AB0372	phosphoribosylam

30	40	41.7	30	2 E71264	hypothetical prote
31	40	41.7	132	2 T46168	thioredoxin-like p
32	40	41.7	156	2 T43834	cytochrome-c oxida
33	40	41.7	181	2 G89799	hypothetical prote
34	40	41.7	183	2 A64248	ribosome releasing
35	40	41.7	183	2 E83447	hypothetical prote
36	40	41.7	229	2 T21714	hypothetical prote
37	40	41.7	324	2 F83426	transcription regu
38	40	41.7	489	2 A96234	sugar ABC transpor
39	40	41.7	489	2 AC3052	hypothetical prote
40	40	41.7	493	2 AB2103	cohyric acid synth
41	40	41.7	531	2 B97040	phage related prot
42	40	41.7	560	2 S27387	interferon alpha r
43	40	41.7	1243	2 T17390	vrkK protein - Dic
44	40	41.7	6658	2 T13931	projectin - fruit
45	39.5	41.1	576	2 AC1384	phosphomannomutase

ALIGNMENTS

RESULT 1

E85508
hypothetical protein Z0260 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E85508
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85508
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-616 <SPO>
A;Cross-references: UNIPROT:Q8X7U6; UNIPARC:UPI00000D09F5; GB:AE005174; NID:gl2512966; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0260
C;Superfamily: uncharacterized conserved protein

Query Match 51.0%; Score 49; DB 2; Length 616;
Best Local Similarity 50.0%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

QY 4 QKVEQFPQ--HGLVK 17
|||:|:|:|:
Db 58 QKIEDEFPPELTHGLIK 73

RESULT 2

E90657
hypothetical protein ECs0229 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E90657
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90657
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-616 <HAY>
A;Cross-references: UNIPROT:Q8X7U6; UNIPARC:UPI00000D09F5; GB:BA000007; PIDN:BAB33652.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs0229
C;Superfamily: uncharacterized conserved protein

Query Match 51.0%; Score 49; DB 2; Length 616;

```
Best Local Similarity 50.0%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDQFPQ--HGLVK 17
   ||:::|::|::|::|
Db 58 QKIEDFPQLTHGLIK 73

RESULT 3
JC7557
lipidosin - mouse
N:Alternate names: lipidosin-related protein
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
A:Accession: JC7557
R:Moriya-Sato, A.; Hida, A.; Inagawa-Ogashiwa, M.; Wada, M.R.; Sugiyama, K.; Shimizu, J.
Biochem. Biophys. Res. Commun. 279, 62-68, 2000
A:Title: Novel acyl-CoA synthetase in adrenoleukodystrophy target tissues.
A:Reference number: JC7557; MUID: 20563802; PMID:11112418
A:Contents: Brain
A:Accession: JC7557
A:Molecule type: mRNA
A:Residues: 1-721 <MOR>
A:Cross-references: UNIPROT:Q99PUS; UNIPARC:UPI000017A518
C:Comment: This protein possesses long-chain acyl-CoA synthetase activity and catalyzes
tion and the impairment of fatty acid metabolism in X-linked adrenoleukodystrophy. This
in human X-linked adrenoleukodystrophy.
C:Keywords: adrenoleukodystrophy

Query Match 49.0%; Score 47; DB 2; Length 721;
Best Local Similarity 53.3%; Pred. No. 8.9;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGL 15
   ||||: : : |||
Db 44 IDGQTLSKESFSHGL 58

RESULT 4
AG3034
inositol monophosphatase family protein [imported] - Agrobacterium tumefaciens (strain C
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
A:Accession: AG3034
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001.
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG3034
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-262 <KUR>
A:Cross-references: UNIPROT:Q8U945; UNIPARC:UPI0000164892; GB:AE008689; PIDN:AAL44693.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3885
A:Map position: linear chromosome
C:Superfamily: suppressor protein subh

Query Match 47.9%; Score 46; DB 2; Length 262;
Best Local Similarity 54.5%; Pred. No. 4.2;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGLV 16
   :::|||||::
Db 59 IEERFPQHGL 69

RESULT 5
```

```
E98251
similar to mlcb1779.29 (probable monophosphatase gene) in mycobacterium leprae [imported]
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
A:Accession: E98251
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurolo, B.; Goldman,
; Goodner, B.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: E98251
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <KUR>
A:Cross-references: UNIPROT:Q8U945; UNIPARC:UPI00000D237F; GB:AE007870; PIDN:AAK89535.1;
C:Genetics:
A:Gene: AGR_L1926
A:Map position: linear chromosome
C:Superfamily: suppressor protein subh

Query Match 47.9%; Score 46; DB 2; Length 297;
Best Local Similarity 54.5%; Pred. No. 4.8;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGLV 16
   :::|||||::
Db 94 IEERFPQHGL 104

RESULT 6
RGBYS3
regulatory protein SIN3 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O2385; protein YOL004w
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1991 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
A:Accession: S66686; A36381; A41957; S12068; S22283
R:Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66685
A:Accession: S66686
A:Molecule type: DNA
A:Residues: 1-1536 <HUG>
A:Cross-references: UNIPROT:P22579; UNIPARC:UPI0000052F61; EMBL:Z74746; NID:gl419766; PI
A:Experimental source: strain S288C
R:Wang, H.; Clark, I.; Nicholson, P.R.; Herskowitz, I.; Stillman, D.J.
Mol. Cell. Biol. 10, 5927-5936, 1990
A:Title: The Saccharomyces cerevisiae SIN3 gene, a negative regulator of HO, contains fo
A:Reference number: A36381; MUID:91042523; PMID:2233725
A:Accession: A36381
A:Molecule type: DNA
A:Residues: 1-510, 'AO', 511-1536 <WAN>
A:Cross-references: UNIPARC:UPI0000168D4F; GB:M36822; NID:gl72093; PIDN:AAA34839.1; PID:
R:Vidal, M.; Strich, R.; Esposito, R.E.; Gaber, R.F.
Mol. Cell. Biol. 11, 6306-6316, 1991
A:Title: RPD1 (SIN3/UME4) is required for maximal activation and repression of diverse y
A:Reference number: A41957; MUID:92049361; PMID:1944290
A:Accession: A41957
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 227-285; 414-441, 'DE', 444-472; 667-725; 1140-1200 <VID>
A:Cross-references: UNIPARC:UPI0000174911; UNIPARC:UPI0000174912; UNIPARC:UPI0000174913;
C:Genetics:
A:Gene: SGD.SIN3; SD11; UME4; RPD1; MIPS.YOL004w
A:Cross-references: SGD:S0005364; MIPS.YOL004w
A:Map position: 15L
C:Superfamily: regulatory protein SIN3
C:Keywords: nucleus; transcription regulation
F:480-519/Region: glutamine-rich

Query Match 46.9%; Score 45; DB 1; Length 1536;
Best Local Similarity 53.3%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

QY 1 IDGQKVDQFPQHGL 15
|||:|||||:
Db 1370 IDGTEVDEEFSPEGI 1384

RESULT 7
T42322
hypothetical protein - phase SPPI
C;Species: phase SPPI
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42322
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of *Bacillus subtilis* strain 168
A;Reference number: Z22137; MUID:98094274; PMID:9434185
A;Accession: T42322
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-105 <ALO>
A;Cross-references: UNIPROT:O48482; UNIPARC:UPI0000009B161; EMBL:X97918; PIDN:CAA66529.1

Query Match 44.8%; Score 43; DB 2; Length 105;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGLVKQ 18
|||:|||||:
Db 5 INQKIGEWIERGRVDQ 22

RESULT 8
G83358
probable ATP-binding component of ABC transporter PA2294 [imported] - *Pseudomonas aeruginosa*
C;Species: *Pseudomonas aeruginosa*
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83358
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brinkman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83358
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-284 <STO>
A;Cross-references: UNIPROT:Q91111; UNIPARC:UPI000000C5650; GB:AE004655; GB:AE004091; NID:1000000000
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2294

Query Match 44.8%; Score 43; DB 2; Length 284;
Best Local Similarity 44.4%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGLVKQ 18
|||:|||||:
Db 73 VDGRSVEGSPQRMVQ 90

RESULT 9
H86717
hypothetical protein ynfB [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C;Species: *Lactococcus lactis* subsp. *lactis*
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86717
R;Boloitin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, G.
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* strain IL1403
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86717
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-654 <STO>
A;Cross-references: UNIPROT:Q9CH17; UNIPARC:UPI000000C68D4; GB:AE005176; PID:gi2723660; P:1000000000
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ynfB

Query Match 44.8%; Score 43; DB 2; Length 654;
Best Local Similarity 43.8%; Pred. No. 39;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGLV 16
|||:|||||:
Db 441 IDHRRDDDFPERALL 456

RESULT 10
D95115
thioredoxin family protein [imported] - *Streptococcus pneumoniae* (strain TIGR4)
C;Species: *Streptococcus pneumoniae*
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95115
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidrich, J.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, C.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: D95115
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-185 <KUR>
A;Cross-references: UNIPROT:Q97R36; UNIPARC:UPI0000051693; GB:AE005672; PIDN:AAK75117.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1000

Query Match 43.8%; Score 42; DB 2; Length 185;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQ 12
|||:|||||:
Db 112 IQGEKTVEQFPQ 123

RESULT 11
H97984
conserved hypothetical protein spr0904 [imported] - *Streptococcus pneumoniae* (strain R6)
C;Species: *Streptococcus pneumoniae*
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: H97984
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Eick, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: H97984
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <KUR>
A;Cross-references: UNIPROT:Q8DQ10; UNIPARC:UPI000000E3552; GB:AE007317; PIDN:AAK99708.1;
C;Genetics:
A;Gene: spr0904

Query Match 43.8%; Score 42; DB 2; Length 191;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQ 12
|||:|||||:

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:22:32 ; Search time 70.1818 Seconds
(without alignments)
237.245 Million cell updates/sec

Title: US-10-758-165a-11
Perfect score: 96
Sequence: 1 IDGQKVDQFPQHGLVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	58.3	245	2	Q3a910_CARHZ
2	51	53.1	1089	2	Q8VQF9_XENBV
3	50.5	52.6	1008	2	Q5GR68_ALCXK
4	50	52.1	271	2	Q450W0_9BURK
5	50	52.1	271	2	Q4LMX1_9BURK
6	50	52.1	283	2	Q88RC3_PSEPK
7	49	51.0	370	2	Q3AGU5_CARHZ
8	49	51.0	616	2	Q3Z5C8_SHISS
9	49	51.0	616	2	Q8X7U6_ECO57
10	48	50.0	345	2	Q61Y77_CAEER
11	48	50.0	442	2	Q43G89_CHLEB
12	48	50.0	851	2	Q2JEG1_9ACTO
13	47.5	49.5	421	2	Q47YD9_COLF3
14	47	49.0	471	2	Q3AX96_SYNG9
15	47	49.0	721	2	Q99PU5_MOUSE
16	47	49.0	724	2	Q6ZQ79_MOUSE
17	46	47.9	239	2	Q87979_BORER
18	46	47.9	239	2	Q7W262_BORFA
19	46	47.9	262	2	Q8U945_AGRFS
20	46	47.9	273	2	Q39U66_GEOGM
21	46	47.9	273	2	Q74BV7_GEOSL
22	46	47.9	297	2	Q7CTJ2_AGRFS
23	46	47.9	331	2	Q3IWI4_RHOS4
24	46	47.9	398	2	Q3PQM7_NITHA
25	46	47.9	608	2	Q8CLW8_YERPE
26	46	47.9	606	2	Q664Y3_YERPS
27	46	47.9	1164	2	Q6SLC8_COCHS
28	45	46.9	201	2	Q75BZ8_ASHGO
29	45	46.9	218	2	Q37VC6_SPHAR
30	45	46.9	342	2	Q5KY10_GEOKA
31	45	46.9	694	2	Q9GZ15_DROME

32 45 46.9 748 2 Q2PYT0_9FUNG
33 45 46.9 783 2 Q7KUY7_DROME
34 45 46.9 840 2 Q9VXL1_DROME
35 45 46.9 970 2 Q4GZA8_9TRYP
36 45 46.9 1536 1 SIN3_YEAST
37 44 45.8 169 2 Q8DKW9_SYNEL
38 44 45.8 243 2 Q3CKR9_THRET
39 44 45.8 282 2 Q65WB1_MANSN
40 44 45.8 376 2 Q54LC6_DICDI
41 44 45.8 386 2 Q6TKU8_ECOLI
42 44 45.8 442 2 Q36PA4_MARHY
43 44 45.8 501 2 Q6ABQ0_PROAC
44 44 45.8 524 2 Q2IKU1_9DELT
45 44 45.8 615 2 Q7N9G7_PHOLL

ALIGNMENTS

RESULT 1

Q3A910_CARHZ PRELIMINARY; PRT; 245 AA.
AC Q3A910;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN OrderedLocusNames=CHY_2581;
OS Carboxydotherrmus hydrogenoformans (strain Z-2901 / DSM 6008).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae;
OC Carboxydotherrmus.
OX NCBI_TaxID=246194;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16311624; DOI=10.1371/journal.pgen.0010065;
RA Wu M., Ren Q., Durkin A.S., Daugherty S.C., Brinkac L.M., Dodson R.J.,
RA Madupu R., Sullivan S.A., Kolonay J.F., Nelson W.C., Taiton L.J.,
RA Jones K.M., Ulrich L.E., Gonzalez J.M., Zhulin I.B., Robb F.T.,
RA Eisen J.A.;
RT "Life in hot carbon monoxide: the complete genome sequence of
RT Carboxydotherrmus hydrogenoformans Z-2901.";
RL PLoS Genet. 1:563-574(2005).

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000141; AB15008.1; -; Genomic_DNA.
DR TIGR; CHY_2581; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 245 AA; 27478 MW; 246C9FE7B62C318D CRC64;

Query Match 58.3%; Score 56; DB 2; Length 245;
Best Local Similarity 44.4%; Pred. No. 1.3;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGLVKQ 18
::: ::: |||:
Db 175 VDGLIEQNFQHGISKQ 192

RESULT 2

Q8VQF9_XENBV PRELIMINARY; PRT; 1089 AA.
ID Q8VQF9_XENBV
AC Q8VQF9;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Peptide synthetase XpsA.
GN Name=xpsA;
OS Xenorhabdus bovienii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Xenorhabdus.
OX NCBI_TaxID=40576;

```

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=T228;
RA Pinyon R.A., Thomas C.J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF455810; AAL57599.1; -; Genomic_DNA.
DR HSP; P14687; IAMU.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA adenyldom.
DR InterPro; IPR009081; ACP-like.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; AMP-bind.
DR InterPro; IPR006163; Phosphopanteth_bd.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00668; Condensation; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR TIGRPFAMS; TIGR01733; AA-adenyl-dom; 1.
DR PROSITE; PS50075; ACP DOMAIN; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 1089 AA; 122987 MW; FF42C1A12506CBF9 CRC64;

Query Match 53.1%; Score 51; DB 2; Length 1089;
Best Local Similarity 53.9%; Pred. No. 40;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 DGQKVDQFPQHQGLVKQ 18
DB 470 DFNKTKPFPQHALIQ 486

RESULT 3
ID Q5GR68_ALCXX PRELIMINARY; PRT; 1008 AA.
AC Q5GR68;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Transposase.
GN Name=tnpA;
OS Alkaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxydans).
OG Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alkaligenaceae; Achromobacter.
OX NCBI_TaxID=85698;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=A8;
RA Jencova V., Strnad H., Chodora Z., Ulbrich P., Hickey W.J., Paces V.;
RT "Chlorocatechol catabolic enzymes from Achromobacter xylosoxydans
RT A8.";
RL Int. Biodeterior. Biodegradation 54:175-181 (2004).
[2]
DR NUCLEOTIDE SEQUENCE.
RP STRAIN=A8;
RA Jencova V.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ515144; CAI47903.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR002513; Transposase_7.
DR Pfam; PF01526; Transposase_7; 1.

```

```

KW Plasmid.
SQ SEQUENCE 1008 AA; 114817 MW; A9F92682878061E5 CRC64;

Query Match 52.6%; Score 50.5; DB 2; Length 1008;
Best Local Similarity 45.5%; Pred. No. 45;
Matches 10; Conservative 3; Mismatches 0; Indels 9; Gaps 1;

QY 1 IDG-----OKVDEQFPQH 13
DB 516 VDGLKQLLTETAEKVDDEFPQH 537

RESULT 4
Q45W0_9BURK PRELIMINARY; PRT; 271 AA.
AC Q45W0;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE ABC transporter.
GN ORFNames=BcndRAFT_2623;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT AU 1054";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAH101000019; EAM11227.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019866; C:organelle inner membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_Arpase.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR02110; ANK.
DR Pfam; PF00005; ABC_tran; 1.
DR PRINTS; PR01415; ANKYRIN.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
SQ SEQUENCE 271 AA; 29686 MW; E3976DF676E02527 CRC64;

Query Match 52.1%; Score 50; DB 2; Length 271;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHQGLVKQ 18

```

```

Db      85 VDGERVDRPHDRGLVQ 102

RESULT 5
Q4LMX1_9BURK
ID      Q4LMX1_9BURK      PRELIMINARY; PRT; 271 AA.
AC      Q4LMX1_
DT      02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT      02-AUG-2005, sequence version 1.
DT      21-FEB-2006, entry version 7.
DE      ABC transporter.
GN      ORFNames=Bcen2424DRAFT_2386;
OS      Burkholderia cenocepacia H12424.
OC      Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC      Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX      NCBI_TaxID=3311272;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=H12424;
RG      US DOE Joint Genome Institute (JGI-PGF);
RA      Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA      Hammon N., Israni S., Pitluck S., Richardson P.;
RT      "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT      H12424."
RL      Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=H12424;
RG      US DOE Joint Genome Institute (JGI-ORNL);
RA      Larimer F., Land M.;
RT      "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT      H12424."
RL      Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC      -1- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
EMBL; AAHL01000041; EAM17437.1; -; Genomic_DNA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0019866; C:organelle inner membrane; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0016987; F:ATPase activity; IEA.
DR      GO; GO:0000166; F:nucleotide binding; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro; IPR003593; AAA_ATPase.
DR      InterPro; IPR003439; ABC_transp_like.
DR      Pfam; PF00005; ABC_tran; 1.
DR      PRINTS; PR01415; ANKYRIN.
DR      ProDom; PD000006; ABC transporter; 1.
DR      SMART; SM00382; AAA; 1.
DR      PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR      PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
SQ      SEQUENCE 271 AA; 29686 MW; E9976DF676E02527 CRC64;

Query Match          52.1%; Score 50; DB 2; Length 271;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 IDGQKVDQFPQHGLVKQ 18
      :||:|||||
Db      85 VDGERVDRPHDRGLVQ 102

RESULT 6
Q88RC3_PSEPK
ID      Q88RC3_PSEPK      PRELIMINARY; PRT; 283 AA.
AC      Q88RC3;
DT      01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT      01-JUN-2003, sequence version 1.

```

```

DT      21-FEB-2006, entry version 23.
DE      Nitrate ABC transporter, ATP-binding protein, putative.
GN      OrderedLocusNames=PP0209; ORFNames=PP_0209;
OS      Pseudomonas putida (strain KT2440).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC      Pseudomonadaceae; Pseudomonas.
OX      NCBI_TaxID=160488;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      MEDLINE=22423060; PubMed=12534463;
RX      DOI=10.1046/j.1462-2920.2002.00366.x;
RA      Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA      Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA      Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA      Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA      Hance I., Chris Lee P., Holtzaple E.K., Scanlan D., Tran K.,
RA      Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA      Wedler H., Lauber J., Stjepandic D., Hobeisel J., Straetz M., Heim S.,
RA      Kiewitz C., Eisen J.A., Fimimis K.N., Duesterhoeft A., Tummeler B.,
RA      Fraser C.M.;
RT      "Complete genome sequence and comparative analysis of the
RT      metabolically versatile Pseudomonas putida KT2440."
RL      Environ. Microbiol. 4:799-808(2002).
CC      -1- SIMILARITY: Belongs to the ABC transporter family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
EMBL; AE015451; AAN65842.1; -; Genomic_DNA.
DR      HSSP; Q9YGA6; 1G29.
DR      TIGR; PP0209; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0016987; F:ATPase activity; IEA.
DR      GO; GO:0000166; F:nucleotide binding; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro; IPR003593; AAA_ATPase.
DR      InterPro; IPR003439; ABC_transp_like.
DR      Pfam; PF00005; ABC_tran; 1.
DR      ProDom; PD000006; ABC transporter; 1.
DR      SMART; SM00382; AAA; 1.
DR      PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR      PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW      ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ      SEQUENCE 283 AA; 31651 MW; DA1B21FCA2223A4A CRC64;

Query Match          52.1%; Score 50; DB 2; Length 283;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 IDGQKVDQFPQHGLVKQ 18
      :||:|||||
Db      73 VDCQPVDPSPQGMVFQ 90

RESULT 7
Q3AG05_CARHZ
ID      Q3AG05_CARHZ      PRELIMINARY; PRT; 370 AA.
AC      Q3AG05;
DT      22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT      22-NOV-2005, sequence version 1.
DT      07-FEB-2006, entry version 4.
DE      Putative serine protease Do.
GN      OrderedLocusNames=CHY_0057;
OS      Carboxydotherrus hydrogeniformans (strain Z-2901 / DSM 6008).
OC      Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae;
OC      Carboxydotherrus.
OX      NCBI_TaxID=246194;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      PubMed=15311624; DOI=10.1371/journal.pgen.0010065;
RA      Wu M., Ren Q., Durkin A.S., Daugherty S.C., Brinkac L.M., Dodson R.J.,
RA      Madupu R., Sullivan S.A., Kolonay J.F., Nelson W.C., Taiton L.J.,

```

```

RA Jones K.M., Ulrich L.E., Gonzalez J.M., Zhulin I.B., Robb F.T.,
RA Eisen J.A.;
RT "Life in hot carbon monoxide: the complete genome sequence of
RT Carboxydotherrmus hydrogenoformans Z-2901.";
RL PLOS Genet. 1:563-574(2005).
CC -1- SIMILARITY: Contains 1 PDZ (DHR) domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000141; ABB15592.1; -; Genomic_DNA.
DR TIGR; CHY 0057; -.
DR GO; GO:0076021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
KW Complete proteome; Hydrolase; Membrane; Protease; Serine protease;
KW Transmembrane.
SQ SEQUENCE 370 AA; 39702 MW; B512C002579F1384 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 370;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVK 18
Db 277 IEQQTIDEEFAQYKGLK 294

RESULT 8
Q325C8 SHISS
ID Q325C8 SHISS PRELIMINARY; PRT; 616 AA.
AC Q325C8
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
GN OrderedLocusNames=SSO_0250; ORFNames=SSO_0250;
OS Shigella sonnei (strain Ss046).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300269;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki1954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000038; AAZ87034.1; -; Genomic_DNA.
DR InterPro; IPRO10272; DUF879_bac.
DR Pfam; PF05947; DUF879; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 616 AA; 71178 MW; 1C4B9A3B0CE75306 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 616;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDEQFPQ--HGLVK 17
Db 58 QKIEDEFPETHGLIK 73

RESULT 9
Q8X7U6_ECO57
ID Q8X7U6_ECO57 PRELIMINARY; PRT; 616 AA.
AC Q8X7U6; Q7AH17;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE No significant matches (Hypothetical protein ECS0229).
GN OrderedLocusNames=ECS0229, 20260;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Rose D.J., Mayhew G.F., Burland V., Mau B., Glasner J.D.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RMD 050952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE005174; AAG54529.1; -; Genomic_DNA.
DR EMBL; BA000007; BAB33652.1; -; Genomic_DNA.
DR PIR; E85508; E85508.
DR PIR; E90657; E90657.
DR BioCyc; ECOL83334-1:ECS0229-MONOMER; -.
DR InterPro; IPRO10272; DUF879_bac.
DR Pfam; PF05947; DUF879; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 616 AA; 71186 MW; 1FBC0A5128341E30 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 616;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDEQFPQ--HGLVK 17
Db 58 QKIEDEFPETHGLIK 73

RESULT 10
Q61Y77_CAEBR
ID Q61Y77_CAEBR PRELIMINARY; PRT; 345 AA.
AC Q61Y77
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein CBG03674.
GN Name=CBG03674;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]

```

```
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RA Stein L.D., Bao Z., Blaslar D., Blumenthal T., Brent M.R., Chen N.,
RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hallier L.W., Kamath R.,
RA Kuwabara P.B., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M.,
RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of Caenorhabditis briggsae: a platform for
RT comparative genomics";
RL PLoS Biol. 1:166-192(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CAAC01000016; CAE60129.1; -; Genomic DNA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 2.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR SMART; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 345 AA; 38450 MW; 744C79ED3D80408D CRC64;

Query Match 50.0%; Score 48; DB 2; Length 345;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 14
:|:|:|
Db 80 VSGKRVDFVQHG 93

RESULT 11
Q43G89_9CHLB PRELIMINARY; PRT; 442 AA.
ID Q43G89;
AC Q43G89;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE Similar to Uncharacterized protein conserved in bacteria.
GN ORFNames=Cpha266DRAFT_1504;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Felodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
```

```
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAI01000015; EAM34597.1; -; Genomic DNA.
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF05990; DUF900; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 442 AA; 48627 MW; 4877E0BFF60B46FC CRC64;

Query Match 50.0%; Score 48; DB 2; Length 442;
Best Local Similarity 64.3%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 14
:|:|:|
Db 390 IDASKVDNGFPQHG 403

RESULT 12
Q2JEG1_9ACTO PRELIMINARY; PRT; 851 AA.
ID Q2JEG1_9ACTO PRELIMINARY; PRT; 851 AA.
AC Q2JEG1;
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DE FHA domain containing protein.
DE PHA domain containing protein.
GN ORFNames=Francis3_0947;
OS Frankia sp. Cc13.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Frankineae; Frankiaceae; Frankia.
OX NCBI_TaxID=106370;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Cc13;
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Goltzman E., Martinez M.,
RA Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A., Francino P.,
RA Benson D.R., Huang Y., Mastromunzio J., Bickhart D., Niemann J.,
RA Rawnsley T., Tisa L.S., Richardson P.;
RA "Complete sequence of Frankia sp. Cc13.";
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000249; ABD10331.1; -; Genomic DNA.
SQ SEQUENCE 851 AA; 92384 MW; B4197D33CA0FD261 CRC64;

Query Match 50.0%; Score 48; DB 2; Length 851;
Best Local Similarity 52.9%; Pred. No. 97;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 17
:|:|:|
Db 66 IDGQRMPEIVPVHGEVR 82

RESULT 13
Q47YD9_COLP3 PRELIMINARY; PRT; 421 AA.
ID Q47YD9_COLP3 PRELIMINARY; PRT; 421 AA.
AC Q47YD9;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE Efflux transporter, RND family, MFP subunit subfamily.
GN OrderedLocusNames=CPS_3507;
OS Colwellia psychrerythraea (strain 34H / ATCC BAA-681) (Vibrio
OS psychrerythrus).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
```

OC Colwelliaceae; Colwellia.
 OX NCBI_TaxID=167879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=16043709; DOI=10.1073/pnas.0504766102;
 RA Meche B.A., Nelson K.E., Deming J.W., Momen B., Melamud E., Zhang X.,
 RA Mault J., Madupu R., Nelson W.C., Dodson R.J., Brinkac L.M.,
 RA Daugherty S.C., Durkin A.S., DeBoy R.T., Kolonay J.F., Sullivan S.A.,
 RA Zhou L., Davidson T.M., Wu M., Huston A.L., Lewis M., Weaver B.,
 RA Weidman J.F., Khouri H., Utterback T.R., Feldblyum T.V., Fraser C.M.;
 RT "The psychrophilic lifestyle as revealed by the genome sequence of
 RT Colwellia psychrerythraea 34H through genomic and proteomic
 RT analyses.";
 RL Proc. Natl. Acad. Sci. U.S.A. 102:10913-10918(2005).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: CP000083; AA226956.1; -; Genomic_DNA.
 DR TIGR; CPS 3507; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008565; F:protein transporter activity; IEA.
 DR GO; GO:0009306; P:protein secretion; IEA.
 DR InterPro; IPR006143; HlyD.
 DR TIGRFAMS; TIGR01730; RND_mfp; 1.
 KW Complete proteome.
 SQ SEQUENCE 421 AA; 47005 MW; 89A1E9649C763790 CRC64;
 Query Match 49.5%; Score 47.5; DB 2; Length 421;
 Best Local Similarity 63.2%; Pred. No. 57;
 Matches 12; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 Yy 1 IDGQKVDQPPQHG-LVYKQ 18
 Db 82 IDGGRVEEVFQEGALVKQ 100
 RESULT 14
 Q3AX96_SYNS9
 ID Q3AX96 SYNS9 PRELIMINARY; PRT; 471 AA.
 AC Q3AX96;
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Arginine decarboxylase (EC 4.1.1.19).
 GN ORFNames=Syncc9902_1380;
 OS Synechococcus sp. (strain CC9902).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=316279;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CC9902;
 RG US DOE Joint Genome Institute;
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Irani S., Pitluck S., Martinez M., Schmutz J., Larimer F.,
 RA Land M., Kyripides N., Ivanova S., Richardson P.;
 RT "Complete sequence of Synechococcus sp. CC9902.";
 RL submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: CP000097; ABB26344.1; -; Genomic_DNA.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0008792; P:arginine decarboxylase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006595; P:polyamine metabolism; IEA.
 KW Lyase.
 SQ SEQUENCE 471 AA; 51718 MW; C9DAA2CAEC3399BD CRC64;
 Query Match 49.0%; Score 47; DB 2; Length 471;
 Best Local Similarity 44.4%; Pred. No. 77;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IDGQKVDQPPQHG-LVYKQ 18
 Db 322 LINGLEADEQPMQGLIAE 339
 RESULT 15
 Q99PU5_MOUSE
 ID Q99PU5_MOUSE PRELIMINARY; PRT; 721 AA.
 AC Q99PU5;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 32.
 DE Lipidosis-related protein Lipidosin (2 days pregnant adult female
 DE oviduct cDNA, RIKEN full-length enriched library, clone:E230019G03
 DE product:lipidosin-related protein lipidosin, full insert sequence)
 DE (Gonadotropin-regulated long chain acyl CoA synthetase).
 GN Name=Acsbgl; Synonyms=Lpd, lpd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=20553802; PubMed=11112418; DOI=10.1006/bbrc.2000.3897;
 RA Moriya-Sato A., Hida A., Inegawa-Ogashiwa M., Wada M.R., Sugiyama K.,
 RA Shimizu J., Yabuki T., Seyama Y., Hashimoto N.;
 RT "Novel acyl-CoA synthetase in adrenoleukodystrophy target tissues.";
 RL Biochem. Biophys. Res. Commun. 279:62-68(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Heminger P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustigich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Humani P., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottaqui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiu K., Sultana R., Takenaka Y., Taki K.,
 RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamashiki H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,

RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.,
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [4]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Oviduct;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RX RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [5]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Oviduct;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RX Okazaki I., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard S., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Santelina A., Schneider C., Sempie C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [6]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Oviduct;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaado I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).

RN NUCLEOTIDE SEQUENCES.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [8]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Oviduct;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [9]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Oviduct;
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurohara C., Matsuyama T., Miyazaki A., Murata M., Kouda M., Koya S.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sodabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Query Match 49.0%; Score 47; DB 2; Length 721;
 Best Local Similarity 53.3%; Pred. No. 1.2e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDGQKVDQPPQHGL 15
 ||||| : : : |||||
 Db 44 IDGQTLKSPSHGL 58

Search completed: August 30, 2006, 04:29:09

Job time : 74.1818 secs

GenCore version 5.1.9
. Copyright (c) 1993 - 2006 Biocellera Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:31:13 ; Search time 17.8182 Seconds
(without alignments)
88.424 Million cell updates/sec

Title: US-10-758-165a-11
Perfect score: 96
Sequence: 1 IDGQKVDQF--POHGLVKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /EMC Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
2: /EMC Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
3: /EMC Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfileseq.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	47.9	195	2	US-09-248-796A-19566
2	45	46.9	1512	2	US-09-328-352-5163
3	45	46.9	1536	2	US-09-487-558B-322
4	43	44.8	612	2	US-09-252-991A-25727
5	42	43.8	137	2	US-08-961-083-40
6	42	43.8	137	2	US-09-536-784-40
7	42	43.8	137	2	US-09-765-271-40
8	42	43.8	137	2	US-09-765-272A-40
9	42	43.8	185	2	US-09-583-110-5222
10	42	43.8	194	2	US-09-107-433-5104
11	42	43.8	228	2	US-09-134-000C-6247
12	42	43.8	359	1	US-08-307-382-2
13	42	43.8	359	1	US-08-366-779-2
14	42	43.8	359	1	US-08-478-777-2
15	42	43.8	359	1	US-08-473-508-2
16	42	43.8	359	1	US-08-789-936-2
17	42	43.8	359	1	US-08-833-610-6
18	42	43.8	359	2	US-08-834-033A-16
19	42	43.8	359	2	US-08-934-254-2
20	42	43.8	359	2	US-09-377-452-6
21	42	43.8	359	2	US-09-685-775-2
22	42	43.8	363	2	US-09-108-020-44
23	42	43.8	363	2	US-09-685-296-44
24	42	43.8	590	2	US-08-489-039A-8178
25	41	42.7	297	2	US-09-248-796A-25364
26	41	42.7	381	2	US-09-248-796A-17552

27	41	42.7	394	2	US-09-252-991A-32539	Sequence 32539, A
28	41	42.7	535	2	US-09-589-733C-18	Sequence 18, Appl
29	41	42.7	536	2	US-09-258-031C-77	Sequence 77, Appl
30	40.5	42.2	246	2	US-09-543-681A-8212	Sequence 8212, Ap
31	40	41.7	230	2	US-09-252-991A-25914	Sequence 25914, A
32	40	41.7	344	2	US-09-252-991A-30083	Sequence 30083, A
33	40	41.7	666	2	US-09-270-767-46736	Sequence 46736, A
34	39.5	41.1	79	2	US-09-248-796A-23915	Sequence 23915, A
35	39.5	41.1	912	1	US-08-951-871-2	Sequence 2, Appli
36	39	40.6	195	2	US-09-252-991A-21451	Sequence 21451, A
37	39	40.6	271	1	US-08-152-019A-28	Sequence 28, Appl
38	39	40.6	336	1	US-07-667-276A-8	Sequence 8, Appli
39	39	40.6	411	2	US-09-134-000C-3961	Sequence 3961, Ap
40	39	40.6	416	2	US-09-134-000C-6248	Sequence 6248, Ap
41	39	40.6	463	2	US-09-198-452A-115	Sequence 115, App
42	39	40.6	468	2	US-09-438-185A-100	Sequence 100, App
43	39	40.6	505	2	US-09-252-991A-29343	Sequence 29343, A
44	39	40.6	510	2	US-09-270-767-46399	Sequence 46399, A
45	39	40.6	1725	2	US-09-562-702A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-248-796A-19566
; Sequence 19566, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19566
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19566

Query Match 47.9% Score 46; DB 2; Length 195;
Best Local Similarity 55.0%; Pred. No. 4.5;
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 IDGQKVDQF--POHGLVKQ 18
:|||||:|
Db 34 MDGQKVDVLLPPQHEIKKQ 53

RESULT 2
US-09-328-352-5163
; Sequence 5163, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GPC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5163
; LENGTH: 1512
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5163

Query Match 46.9%; Score 45; DB 2; Length 1512;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GQKVDQEQPQHGLVKQ 18
Db 328 GDRDPLMPHSHGLVSQ 343

RESULT 3
US-09-487-558B-322
; Sequence 322, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 322
; LENGTH: 1536
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-322

Query Match 46.9%; Score 45; DB 2; Length 1536;
Best Local Similarity 53.3%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQEQPQHGL 15
Db 1370 IDGTEVDEEFSPEGI 1384

RESULT 4
US-09-252-991A-25727
; Sequence 25727, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25727
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25727

Query Match 44.8%; Score 43; DB 2; Length 612;

Best Local Similarity 44.4%; Pred. No. 55;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IDGQKVDQEQPQHGLVKQ 18
Db 401 VDGRSVEGSPQRGMVFQ 418

RESULT 5
US-08-961-083-40
; Sequence 40, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELEPHONE: (301) 309-8504
; TELEPHONE: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-40

Query Match 43.8%; Score 42; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQEQPQ 12
Db 93 IQGEKTEQPPQ 104

RESULT 6
US-09-536-784-40
; Sequence 40, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland

; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-536-784-40

Query Match 43.8%; Score 42; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQ 12
|:|:|:|:|:|
Db 93 IQEKTVEQFPQ 104

RESULT 7
US-09-765-271-40
; Sequence 40, Application US/09765271
; Patent No. 6887663
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,271
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/536,784
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-765-271-40
Query Match 43.8%; Score 42; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQ 12
|:|:|:|:|:|
Db 93 IQEKTVEQFPQ 104

RESULT 8
US-09-765-272A-40
; Sequence 40, Application US/09765272A
; Patent No. 6929930
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 454
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: Dell Latitude C610
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272A
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin J. Hymel
; REGISTRATION NUMBER: 45,414
; REFERENCE/DOCKET NUMBER: PB340P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-765-272A-40

Query Match 43.8%; Score 42; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQ 12
|:|:|:|:|:|

Db 93 IQGKTVQPPQ 104

RESULT 9

US-09-583-110-5222

Sequence 5222, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

FILE REFERENCE: PATH00-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 5222

LENGTH: 185

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-583-110-5222

Query Match 43.8%; Score 42; DB 2; Length 185;

Best Local Similarity 66.7%; Pred. No. 21;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQPPQ 12

Db 112 IQGKTVQPPQ 123

RESULT 10

US-09-107-433-5104

Sequence 5104, Application US/09107433

Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneka

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 5104:

SEQUENCE CHARACTERISTICS:

LENGTH: 194 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...194

SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

US-09-107-433-5104

Query Match 43.8%; Score 42; DB 2; Length 194;

Best Local Similarity 66.7%; Pred. No. 22;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IDGQKVDQPPQ 12

Db 121 IQGKTVQPPQ 132

RESULT 11

US-09-134-000C-6247

Sequence 6247, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patent in version 3.1

SEQ ID NO 6247

LENGTH: 228

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-6247

Query Match 43.8%; Score 42; DB 2; Length 228;

Best Local Similarity 87.5%; Pred. No. 26;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FPOHGLVK 17

Db 174 FPOHGLVK 181

RESULT 12

US-08-307-382-2

Sequence 2, Application US/08307382

Patent No. 5552306

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

APPLICANT: Reddy, Avutu S.

APPLICANT: Nuccio, Michael

APPLICANT: Freyssinet, Georges L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC

TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,382
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/817,919
; FILING DATE: 08-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McNulty, William E.
; REGISTRATION NUMBER: 22,606
; REFERENCE/DOCKET NUMBER: 8383Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-307-382-2

Query Match 43.8%; Score 42; DB 1; Length 359;
Best Local Similarity 46.7%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 QKVDEQFPQHGLVKQ 18
Db 21 QRVDAYFAEHLTOR 35

RESULT 13
US-08-366-779-2
; Sequence 2, Application US/08366779
; Patent No. 5614393
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,779
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
```

```
;
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-366-779-2

Query Match 43.8%; Score 42; DB 1; Length 359;
Best Local Similarity 46.7%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 QKVDEQFPQHGLVKQ 18
Db 21 QRVDAYFAEHLTOR 35

RESULT 14
US-08-478-727-2
; Sequence 2, Application US/08478727
; Patent No. 5663068
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,727
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,382
; FILING DATE: 14-SEP-1994
; APPLICATION NUMBER: US 07/817,919
; FILING DATE: 08-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McNulty, William E.
; REGISTRATION NUMBER: 22,606
; REFERENCE/DOCKET NUMBER: 8383Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-478-727-2

Query Match 43.8%; Score 42; DB 1; Length 359;
Best Local Similarity 46.7%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 QKVDEQFPQHGLVKQ 18
Db 21 QRVDAYFAEHLTOR 35
```

Search completed: August 30, 2006, 04:33:00
Job time : 18.8182 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:33:28 ; Search time 90.9091 Seconds
(without alignments)
91.717 Million cell updates/sec

Title: US-10-758-165a-11
Perfect score: 96
Sequence: 1 IDGQKVDQPPQHGVLVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	5	US-10-758-165-11
2	96	100.0	424	4	US-10-451-078-2
3	96	100.0	424	4	US-10-451-078-4
4	78	81.2	15	4	US-10-052-788-5
5	63	65.6	569	4	US-10-214-524-30
6	45	46.9	178	4	US-10-424-599-146307
7	45	46.9	504	4	US-10-282-122A-55836
8	45	46.9	685	6	US-11-037-143-19596
9	45	46.9	1536	3	US-09-801-368-322
10	44	45.8	89	4	US-10-424-599-205669
11	44	45.8	128	5	US-10-450-763-36065
12	44	45.8	130	4	US-10-424-599-145103
13	44	45.8	159	5	US-10-450-763-36064
14	44	45.8	387	4	US-10-437-963-154933
15	44	45.8	421	4	US-10-238-075-1472
16	43.5	45.3	718	4	US-10-017-161-784
17	43	44.8	70	6	US-11-188-298-3776
18	43	44.8	121	4	US-10-425-115-187877
19	43	44.8	146	4	US-10-425-114-46519
20	43	44.8	149	4	US-10-425-115-210792
21	43	44.8	152	4	US-10-425-114-42340
22	43	44.8	316	5	US-10-922-282-12
23	43	44.8	325	4	US-10-425-114-37611
24	43	44.8	346	4	US-10-425-114-39926
25	43	44.8	356	5	US-10-922-282-30
26	43	44.8	366	4	US-10-425-114-37769
27	43	44.8	371	4	US-10-425-114-48824

28	43	44.8	374	4	US-10-767-701-45372	Sequence 45372, A
29	43	44.8	374	4	US-10-425-115-216179	Sequence 216179, A
30	43	44.8	374	4	US-10-425-115-216182	Sequence 216182, A
31	43	44.8	375	4	US-10-767-701-42582	Sequence 42582, A
32	43	44.8	398	4	US-10-425-115-300080	Sequence 300080, A
33	43	44.8	403	4	US-10-425-114-40459	Sequence 40459, A
34	43	44.8	403	4	US-10-425-114-57233	Sequence 57233, A
35	43	44.8	409	4	US-10-425-114-46619	Sequence 46619, A
36	43	44.8	434	4	US-10-437-963-169342	Sequence 169342, A
37	43	44.8	605	4	US-10-424-599-157014	Sequence 157014, A
38	42	43.8	84	4	US-09-765-272-40	Sequence 40, Appl
39	42	43.8	137	3	US-11-106-649-40	Sequence 40, Appl
40	42	43.8	137	6	US-10-472-528-1980	Sequence 1980, Ap
41	42	43.8	185	5	US-10-474-776-661	Sequence 661, App
42	42	43.8	191	4	US-10-617-320-5104	Sequence 5104, Ap
43	42	43.8	194	5	US-10-282-122A-46126	Sequence 46126, A
44	42	43.8	199	4	US-10-369-493-2768	Sequence 2768, Ap
45	42	43.8	218	4		

ALIGNMENTS

RESULT 1
US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match 100.0%; Score 96; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDQPPQHGVLVKQ 18
Db 1 IDGQKVDQPPQHGVLVKQ 18

RESULT 2
US-10-451-078-2
; Sequence 2, Application US/10451078
; Publication No. US20040115764A1
; GENERAL INFORMATION:
; APPLICANT: Leibold, Wolfgang
; APPLICANT: Bettina, Wagner
; APPLICANT: Radbruch, Andreas

; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the Heavy Chain of an Equine IgE Allotype, Recombinant Immunoglobulins Obtained Using Them, and Corresponding Isotype-specific Monoclonal Antibodies and their Use
; FILE REFERENCE: 03100177aa
; CURRENT APPLICATION NUMBER: US/10/451,078
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: PCT/DE01/04810
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 100 64 415.5
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2

SEQ ID NO 2
LENGTH: 424
TYPE: PRT
ORGANISM: Equus caballus
FEATURE:
NAME/KEY: Domain
LOCATION: (1)..(97)
OTHER INFORMATION: CH1 domain, IgE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (98)..(205)
OTHER INFORMATION: CH2 domain, IgE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (206)..(312)
OTHER INFORMATION: CH3 domain, IgE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (313)..(424)
OTHER INFORMATION: CH4 domain, IgE allotype a
US-10-451-078-2

Query Match 100.0%; Score 96; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVKQ 18
Db 145 IDGQKVDQFPQHGVLVKQ 162

RESULT 3
US-10-451-078-4
Sequence 4, Application US/10451078
Publication No. US20040115764A1
GENERAL INFORMATION:
APPLICANT: Leibold, Wolfgang
APPLICANT: Bettina, Wagner
APPLICANT: Radbruch, Andreas
TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the Heavy Chain of an Equine IgE Allotype, Recombinant
TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
FILE REFERENCE: 03100177aa
CURRENT APPLICATION NUMBER: US/10/451,078
CURRENT FILING DATE: 2003-12-24
PRIOR APPLICATION NUMBER: PCT/DE01/04810
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: DE 100 64 415.5
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 424
TYPE: PRT
ORGANISM: Equus caballus
FEATURE:
NAME/KEY: Domain
LOCATION: (1)..(97)
OTHER INFORMATION: CH1 domain, IgE allotype b
FEATURE:
NAME/KEY: Domain
LOCATION: (98)..(205)
OTHER INFORMATION: CH2 domain, IgE allotype b
FEATURE:
NAME/KEY: Domain
LOCATION: (206)..(312)
OTHER INFORMATION: CH3 domain, IgE allotype b
FEATURE:
NAME/KEY: Domain
LOCATION: (313)..(424)
OTHER INFORMATION: CH4 domain, IgE allotype b
US-10-451-078-4

Query Match 100.0%; Score 96; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVKQ 18
Db 145 IDGQKVDQFPQHGVLVKQ 162

RESULT 4
US-10-052-788-5
Sequence 5, Application US/10052788
Publication No. US20030087314A1
GENERAL INFORMATION:
APPLICANT: Gershwin, Laurel J.
APPLICANT: Pettigrew, Howard David
APPLICANT: Kalina, Warren V.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for Induction of Anti-IgE Antibodies
FILE REFERENCE: 023070-121000US
CURRENT APPLICATION NUMBER: US/10/052,788
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: epitope peptide
OTHER INFORMATION: P5, middle portion of C2 of equine IgE epsilon chain
OTHER INFORMATION: heavy chain
US-10-052-788-5

Query Match 81.2%; Score 78; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHG 14
Db 2 IDGQKVDQFPQHG 15

RESULT 5
US-10-214-524-30
Sequence 30, Application US/10214524
Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Swei-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REFERENCE: ICE-00101.P.1-1
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 569
TYPE: PRT
ORGANISM: Horse (Equus caballus)
US-10-214-524-30

Query Match 65.6%; Score 63; DB 4; Length 569;
Best Local Similarity 66.7%; Pred. No. 0.13;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVKQ 18

```
Db      291  IEGQKVDQFPPTQASMKQ 308
          |||:|||||:|
RESULT 6
US-10-424-599-146307
; Sequence 146307, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146307
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_103132C.1.pcp
US-10-424-599-146307
Query Match      46.9%; Score 45; DB 4; Length 178;
Best Local Similarity 57.1%; Pred. No. 34;
Matches      8; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

QY      1  IDGQKVDQFPQHG 14
          |||:|||||:|
Db      152  VDSNVAPQFPQHG 165

RESULT 7
US-10-282-122A-55836
; Sequence 55836, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

US-10-097-143-19596
; Sequence 19596, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19596
; LENGTH: 685
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-19596
Query Match      46.9%; Score 45; DB 6; Length 685;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches      8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3  GQKVDEQFPQHG 17
          |||:|||||:|
Db      577  GQVGSNSYPERGLVK 591

RESULT 9
US-09-801-368-322
; Sequence 322, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
```

```
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55836
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-55836
Query Match      46.9%; Score 45; DB 4; Length 504;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches      8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  IDGQKVDQFPQHG 15
          |||:|||||:|
Db      315  IDGERVDIQPAHAI 329

RESULT 8
US-11-097-143-19596
; Sequence 19596, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19596
; LENGTH: 685
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-19596
Query Match      46.9%; Score 45; DB 6; Length 685;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches      8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3  GQKVDEQFPQHG 17
          |||:|||||:|
Db      577  GQVGSNSYPERGLVK 591

RESULT 9
US-09-801-368-322
; Sequence 322, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
```

APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250Alman, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801.368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 322
LENGTH: 1536
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-322

Query Match 46.9%; Score 45; DB 3; Length 1536;
Best Local Similarity 53.3%; Pred. No. 3.8e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGL 15
Db 1370 IDGTEVDEEFSPEGI 1384

RESULT 10
US-10-424-599-205669
Sequence 205669, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205669
LENGTH: 89
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(89)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_27747C.1.pep
US-10-424-599-205669

Query Match 45.8%; Score 44; DB 4; Length 89;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GQKVDQFPQHG 14
Db 46 GIKMDRMPQHG 57

RESULT 11
US-10-450-763-36065
Sequence 36065, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hysq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 36065
LENGTH: 128
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(128)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-36065

Query Match 45.8%; Score 44; DB 5; Length 128;
Best Local Similarity 52.9%; Pred. No. 35;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DGQKVDQFPQHGLVKQ 18
Db 60 DPQPREQSPVHGLVQR 76

RESULT 12
US-10-424-599-145103
Sequence 145103, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 145103
LENGTH: 130
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_102046C.1.pep
US-10-424-599-145103

Query Match 45.8%; Score 44; DB 4; Length 130;
Best Local Similarity 69.2%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKVDQFPQHGL 15
Db 65 GQLQAELEFPQHGL 77

RESULT 13
US-10-450-763-36064
Sequence 36064, Application US/10450763

; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36064
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(159)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-36064

Query Match 45.8%; Score 44; DB 5; Length 159;
Best Local Similarity 52.9%; Pred. No. 45;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DGKVDQFPQHGVLVKQ 18
Db 91 DPQRPQSPVHGLVQR 107

RESULT 14

US-10-437-963-154933
; Sequence 154933, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 154933
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54746C.1.pep
US-10-437-963-154933

Query Match 45.8%; Score 44; DB 4; Length 387;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15
Db 302 IEESFPQHGI 311

RESULT 15

US-10-238-075-1472
; Sequence 1472, Application US/10238075

; Publication No. US20030148324A1
; GENERAL INFORMATION:
; APPLICANT: I.N.S.E.R.M.
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
; FILE REFERENCE: BLANDINE
; CURRENT APPLICATION NUMBER: US/10/238,075
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0003145
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1472
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-1472

Query Match 45.8%; Score 44; DB 4; Length 421;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 7; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDEQFPQ--HGLVK 17
Db 58 QKLEDEFPFTHGLIR 73

Search completed: August 30, 2006, 05:12:59
Job time : 91.9091 secs

This Page Blank (uspto)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 04:34:57 ; Search time 9.27273 Seconds
(without alignments)
133.695 Million cell updates/sec

Title: US-10-758-165a-11

Perfect score: 96

Sequence: 1 IDGQKVDQPPQHGLVKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US09_NEW_PUB.pap:*
- 2: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pap:*
- 3: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pap:*
- 4: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pap:*
- 5: /EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.pap:*
- 6: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US10_NEW_PUB.pap:*
- 7: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US11_NEW_PUB.pap:*
- 8: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	45.8	356	6	US-10-449-902-33028
2	44	45.8	376	6	US-10-449-902-47548
3	43	44.8	321	7	US-11-056-355B-6060
4	43	44.8	373	7	US-11-056-355B-6059
5	43	44.8	374	7	US-11-174-307B-286
6	43	44.8	400	7	US-11-174-307B-288
7	43	44.8	448	7	US-11-056-355B-6058
8	42	43.8	273	6	US-10-449-902-30777
9	42	43.8	314	7	US-11-056-355B-26554
10	42	43.8	314	7	US-11-056-355B-108652
11	42	43.8	314	7	US-11-056-355B-119891
12	42	43.8	328	6	US-10-953-349-26705
13	42	43.8	328	7	US-11-056-355B-26553
14	42	43.8	328	7	US-11-056-355B-68215
15	42	43.8	328	7	US-11-056-355B-108651
16	42	43.8	328	7	US-11-056-355B-119890
17	42	43.8	351	6	US-10-953-349-26704
18	42	43.8	351	7	US-11-056-355B-68214
19	42	43.8	353	7	US-11-330-403-2110
20	42	43.8	363	7	US-11-174-307B-2812
21	42	43.8	363	7	US-11-056-355B-26552
22	42	43.8	363	7	US-11-056-355B-108650
23	42	43.8	363	7	US-11-056-355B-119889
24	42	43.8	366	6	US-10-953-349-26703
25	42	43.8	366	7	US-11-056-355B-68213

26	41	42.7	286	7	US-11-056-355B-26724	Sequence 26724, A
27	41	42.7	286	7	US-11-056-355B-74037	Sequence 74037, A
28	41	42.7	477	7	US-11-330-403-7987	Sequence 7987, Ap
29	40	41.7	132	6	US-10-952-500-167	Sequence 167, App
30	40	41.7	292	7	US-11-330-403-11936	Sequence 11936, A
31	40	41.7	393	6	US-10-449-902-37067	Sequence 37067, A
32	40	41.7	415	7	US-11-056-355B-89336	Sequence 89336, A
33	40	41.7	415	7	US-11-056-355B-93092	Sequence 93092, A
34	40	41.7	455	7	US-11-056-355B-89335	Sequence 89335, A
35	40	41.7	455	7	US-11-056-355B-93091	Sequence 93091, A
36	40	41.7	469	7	US-11-056-355B-89334	Sequence 89334, A
37	40	41.7	469	7	US-11-056-355B-93090	Sequence 93090, A
38	39.5	41.1	576	7	US-11-330-403-4484	Sequence 4484, Ap
39	39	40.6	297	6	US-10-953-349-20831	Sequence 20831, A
40	39	40.6	299	6	US-10-953-349-20830	Sequence 20830, A
41	39	40.6	323	7	US-11-056-355B-30253	Sequence 30253, A
42	39	40.6	323	7	US-11-056-355B-30764	Sequence 30764, A
43	39	40.6	323	7	US-11-056-355B-33843	Sequence 33843, A
44	39	40.6	323	7	US-11-056-355B-34354	Sequence 34354, A
45	39	40.6	328	6	US-10-449-902-39837	Sequence 39837, A

ALIGNMENTS

RESULT 1

US-10-449-902-33028
; Sequence 33028, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 33028
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33028

Query Match 45.8%; Score 44; DB 6; Length 356;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15
Db 282 IEESFPQHG 291

RESULT 2

US-10-449-902-47548
; Sequence 47548, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269

```
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47548
; LENGTH: 376
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-47548

Query Match      45.8%; Score 44; DB 6; Length 376;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      6 VDEQFPQHGL 15
Db      302 IEESFPQHGI 311

RESULT 3
US-11-056-355B-6060
; Sequence 6060, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 6060
; LENGTH: 321
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(321)
; OTHER INFORMATION: Ceres Seq. ID no. 12344159
US-11-056-355B-6060

Query Match      44.8%; Score 43; DB 7; Length 321;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      6 VDEQFPQHGL 15
Db      246 VEEGFPQHGI 255

RESULT 4
US-11-056-355B-6059
; Sequence 6059, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 6059
; LENGTH: 373
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
```

```
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(373)
; OTHER INFORMATION: Ceres Seq. ID no. 12344158
US-11-056-355B-6059

Query Match      44.8%; Score 43; DB 7; Length 373;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      6 VDEQFPQHGL 15
Db      298 VEEGFPQHGI 307

RESULT 5
US-11-174-307B-286
; Sequence 286, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174.307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 286
; LENGTH: 374
; TYPE: prt
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Transket_pyr; Pfam Description: Transketolase,
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Transketolase_C; Pfam Description: Transketolase,
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 520478; NR Description: pyruvate dehydrogenase E1
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3850999; NR Description: pyruvate dehydrogenase E1
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3851001; NR Description: pyruvate dehydrogenase E1
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 3851003; NR Description: pyruvate dehydrogenase E1
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 25012844; NR Description: RH05604p [Drosophila
US-11-174-307B-286

Query Match      44.8%; Score 43; DB 7; Length 374;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      6 VDEQFPQHGL 15
```

RESULT 7
US-11-056-355B-6058
; Sequence 6058, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai

```

RESULT 9
US-11-056-355B-26554
; Sequence 26554, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14

```

; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 26554
; LENGTH: 314
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(314)
; OTHER INFORMATION: Ceres Seq. ID no. 12384700
US-11-056-355B-26554

Query Match 43.8%; Score 42; DB 7; Length 314;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15
|:|||||:
Db 246 VEEGFPQHG 255

RESULT 10

US-11-056-355B-108652
; Sequence 108652, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: Polypeptides Encoded Thereby
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 108652
; LENGTH: 314
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(314)
; OTHER INFORMATION: Ceres Seq. ID no. 13668006
US-11-056-355B-108652

Query Match 43.8%; Score 42; DB 7; Length 314;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15
|:|||||:
Db 246 VEEGFPQHG 255

RESULT 11

US-11-056-355B-119891
; Sequence 119891, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: Polypeptides Encoded Thereby
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 119891
; LENGTH: 314

; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(314)
; OTHER INFORMATION: Ceres Seq. ID no. 13668006
US-11-056-355B-119891

Query Match 43.8%; Score 42; DB 7; Length 314;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15
|:|||||:
Db 246 VEEGFPQHG 255

RESULT 12

US-10-953-349-26705
; Sequence 26705, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THEREBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26705
; LENGTH: 328
; TYPE: PRt
; ORGANISM: Triticum aestivum
US-10-953-349-26705

Query Match 43.8%; Score 42; DB 6; Length 328;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15
|:|||||:
Db 260 VEEGFPQHG 269

RESULT 13

US-11-056-355B-26553
; Sequence 26553, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: Polypeptides Encoded Thereby
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 26553
; LENGTH: 328
; TYPE: Prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(328)
; OTHER INFORMATION: Ceres Seq. ID no. 12384699
US-11-056-355B-26553

Query Match 43.8%; Score 42; DB 7; Length 328;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Search completed: August 30, 2006, 04:35:56
Job time : 9.27273 secs

Qy 6 VDEQFPQHGL 15
|:|:|:|:|:
Db 260 VEGFPQHG 269

RESULT 14

US-11-056-355B-68215
; Sequence 68215, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 68215
; LENGTH: 328
; TYPE: prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(328)
; OTHER INFORMATION: Ceres Seq. ID no. 13596007
US-11-056-355B-68215

Query Match 43.8%; Score 42; DB 7; Length 328;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15
|:|:|:|:|:
Db 260 VEGFPQHG 269

RESULT 15

US-11-056-355B-108651
; Sequence 108651, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 108651
; LENGTH: 328
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(328)
; OTHER INFORMATION: Ceres Seq. ID no. 13668005
US-11-056-355B-108651

Query Match 43.8%; Score 42; DB 7; Length 328;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VDEQFPQHGL 15
|:|:|:|:|:
Db 260 VEGFPQHG 269

This Page Blank (uspto)